4	5	14	13	24	28	33	38
66c 61y	AAG Lys	GGT Gly	CAC	666 617	TCA Ser	GCT Ala	ACT Thr
CCG	TCC Ser	GGT	GGT Gly	ATG Met	TAT TYE	GCC	GGC Gly
CCC	CT'C Leu	ATG Met	AAG Lys	AAC Asn	AAC Asn	GCT	GGA Gly
GAT Asp	CGC	GGA Gly	GAG	ACA	CCA Pro	CAT	SCT
GTG Val	GAC Asp	ACA T'hr	Nrc Ile	ATT	66C Gly	rrc	A1G A1'F G Met Ile A
CTA	GCC	GGA	CTT	GCC	ATG Met	rcc	ATG Met
GAA	GGT Gly	GTC Val	TCT	TAT Tyr	CTC	TAC	CTYF
CTA	CTC	CTG	CAG Gln	CCC	GG'r Gly	AAC Asn	GAT Asp
GC'r Ala	GAT Asp	GTG Val	GTT Val	ATC Ile	rrr Phe	TCC	GCT
GCC	GCC Ala	GGA	GGG Gly	TTC	GAA Glu	ACT Thr	GAG Glu
GCG Ala	CGA	GCC Ala	GAC Asp	TTC Phe	NTC Ile	GCC	GGT Gly
GT'G Val	GCA	AGA	TCT Ser	CCT	GCT	TGT Cys	CGT
GCG	TCG	GAG Glu	TTC	ACC	CTC Leu	GCA	CGC
ACC Thr	AA'I' Asn	AAG Lys	Grc Val	ATC Ile	CTG	ACT Thr	ATC Ile
7CC Ser	NGG Arg	GAC Asp	AC'r Thr	AAA Lys	GCC	TCC	CAT His
AGC	TGC Cys	ATC	CTG	CGG Arg	TC'r Ser	A'IT Ile	AAT Asn

ထ

FIGURE 1

40	\$ 2	57	62	67	72
TGG Trp	1'rG Leu	ΛΊΤ΄ Ile	ACT Thr	AGC	GCT Ala
CCC	GTG Val	ATT Ile	ATG	AGT Ser	M.T Asn
agg	GGA G1y	CCG	CAC	GAG Glu	GTC AAT TAC ATA Val Asn Tyr Ile
T'C'r Ser	GCT	GCA Ala	TAT Tyr	AT'T Ile	TAC Tyr
GCC	GGT Gly	GGA Gly		TGC	AAT' Asn
	GAA Glu	CGA	Gat Asp	TCT Ser	GTC Val
	GGT Gly	AGA Arg	TGT Cys	TCT Ser	GAG Glu
CCG	ATG Met	ATG Met	AAC Asn	GTC Val	GAA
	GT'G Val	GCA Ala	nic Ile	GG'r Gly	CCT
	'r'r'' Phe	CAT	GCA	CTT Leu	TCA
	GGT Gly	GAA	GGT G1y	$_{\rm GGT}^{\rm GGT}$	Grc Val
AGG Arg	GAT	TTG	gga gly	GAT Asp	66C G1y
	CGT	AGC	TTG	GCT Ala	GC'r Ala
	GAC Asp	GAG	TAT Tyr	AGG Arg	GAT Asp
TTG	AAA Lys	ATG Met	GAG	CCA Pro	GAA Glu
GCT	GAT Asp	GTG	GCA	GAT Asp	CTT Leu
	TTG TCT CAA AGG AAC GAT GAC CCG CAG ACT GCC TCT AGG CCC TGG Lew Ser Gln Arg Asn Asp Asp Pro Gln Thr Ala Ser Arg Pro Trp	TTG TCT CAA AGG AAC GAT GAC CCG CAG ACT GCC TCT AGG CCC TGG Lew Ser Gln Arg Asn Asp Asp Pro Gln Thr Ala Ser Arg Pro Trp AAA GAC CGT GAT GGT TTT GTG ATG GGT GAA GGT GCT GGA GTG TTG Lys Asp Arg Asp Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu	TTG TCT CAA AGG AAC GAT GAC CCG CAG ACT GCC TCT AGG CCC TGG Lew Ser Gln Arg Asn Asp Asp Pro Gln Thr Ala Ser Arg Pro Trp AAA GAC CGT GAT GGT TTT GTG ATG GGT GAT GCT GGA GTG TTG Lys Asp Arg Asp Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu ATG GAG AGC TTG GAA CAT GCA ATG AGA CGA GGA GCA CCG ATT ATT Met Glu Ser Leu Glu His Ala Met Arg Arg Gly Ala Pro Ile Ile	TTG TCT CAA AGG AAC GAT GAC CCG CAG ACT GCC TCT AGG CCC TGG Leu Ser Gln Arg Asn Asp Asp Pro Gln Thr Ala Ser Arg Pro Trp AAA GAC CGT GAT GGT TTT GTG ATG GGT GAA GGT GCT GGA GTG TTG Lys Asp Arg Asp Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu ATG GAG AGC TTG GAA CAT GCA ATG AGA CGA GGA GCA CCG ATT ATT Met Glu Ser Leu Glu His Ala Met Arg Arg Gly Ala Pro Ile Ile GAG TAT TTG GGA GGT GCA ATC AAC TGT GAT GCT TAT CAC ATG ACT GTU Tyr Leu Gly Gly Ala Ile Asn Cys Asp Ala Tyr His Met Thr	TTG TCT CAA AGG AAC GAT GAC CCG CAG ACT GCC TCT AGG CCC TGG Leu Ser Gln Arg Asn Asp Asp Pro Gln Thr Ala Ser Arg Pro Trp AAA GAC GT GAT GGT TTT GTG ATG GGT GAA GGT GCT GGA GTG TTG Lys Asp Arg Asp Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu ATG GAG AGC TTG GAA CAT GCA ATG AGA CGA GGA GCA CCG ATT ATT Met Glu Ser Leu Glu His Ala Met Arg Arg Gly Ala Pro 11e 11e GAG TAT TTG GGA GGT GCA ATC AAC ASP ASP Ala TYT GAS ACT Glu Tyr Leu Gly Gly Ala 11e Asn Cys Asp Ala Tyr His Met Thr CCA AGG GCT GAT GGT CTT GGT GTC TCT TGC ATT GAG AGT AGC Pro Arg Ala Asp Gly Leu Gly Val Ser Ser Cys 11e Glu Ser Ser

FIGURE 1 2/4

768	816	864	912	096	1008	1056
GAG ATA AAT GCC ATC	ATT AAT GCA ACT AAG	GGT C'I'I GAA GCT' ATA	CAT CCC AGC ATT AAT	ACT GTT GCC AAC AAG	AAT TCA TTC GGA TTT	TTC AAG CCA TGATTA
Glu Ile Asn Ala Ile	Ile Asn Ala Thr Lys	Gly Leu Glu Ala Ile	His Pro Ser Ile Asn	Thr Val Ala Asn Lys	Asn Ser Phe Gly Phe	Phe Lys Pro
CTC GCC	ATC AAA	TCT GGA	TGG CTT	rrc GAC	ATC TCG	TCG GCT
Leu Ala	Ile Lys	Ser Gly	Trp Leu	Phe Asp	Ile Ser	Ser Ala
GGG GA'F	AAG GAT	GGN GCN	ACC GGC	GTG GAG	GTT GCG	GCT 1YC
Gly Asp	Lys Asp	Gly Nla	Thr Gly	Val Glu	Val Ala	Ala Phe
CTA GCT	NAC ACA	TGT CTT	ATA AAC	CCA TCG	GTT AAC	G'TC G'TG
Leu Ala	Asn Thr	Cys Leu	Ile Asn	Pro Ser	Val Asn	Val Val
TCT ACT	TTC AAG	GGA CAC	AAG GGA	CCT GAG	CAC GAA	AAC TCA
Ser Thr	Phe Lys	Gly His	Lys Gly	Pro Glu	His Glu	Asn Ser
CAT GCG ACT	AAG, AAG GIT	TCA ATG ATC	GCG ACT ATT	CAA TTC AAT	AAG CAG CAA	GGA GGC CAC
His Ala Thr	Lys Lys Val	Ser Met Ile	Ala Thr Ile	Gln Phe Asn	Lys Gln Gln	Gly Gly His
					7 -	

FIGURE 1 3/4

CCCATITICAC	CCCNITICAC AAGGIACITG TCATIGAGAA 1'ACGGAI'FAI' GGACITGCAG AGIFAAT'ITCC	TCATTGAGAA	TYACGGAT*FAT	GGACTTGCAG	AGTAATTTCC	1116
ccatgrangr	CCATGITIGI CGGAAGAGCA TATIACCACG GITGICCGIC AMCCCATIII AGGATACIGI	TATTACCACG	GITGICCGIC	AMCCCATIT	AGGATACTGT	1176
TCTATGTAAT	ICTATIGIAAT AAAACTAAGG ATTATITITAATTI TCCCTTTTIAA TCCTGTCTCC AGITTGAGCA	יויויהאזיזיגידיה	rcccrrrrin	recrerence	AGIITTGAGCA	1236
TGAAATTATA	TGAAATTATA TYYATYYYAT CYYAGAAAGG YCAAAYAAAGA TYYYGYYYYA CCTCTGTAAA	C'FFAGAAAGG	TCAMATANGA	TYTTYTG'FTYFFA	CCTCTGTAAA	1296
ACTTITITITI	ACTITITICITIT GIATITGGAAA GGAAGIGCCG ICTCAAAAAA AAAAAAAAA AA	GGAAGTGCCG	TCTCAAAAAA	ANNNAMANAN	\$	1348

FIGURE 1 4/4

Sequence Range: 1 to 1704

40 GTG Val>		GCA Ala>		TCT Ser>	190	GAC Asp>	240	CGG Arg>	CTC Leu>		GAA Glu>
GNG		TCG	140	GAC	7	ATC Ile		ATC Ile	AGG Arg		C'rc Leu
ACC	90	AAT	-	GTC Val		TTA		CAG Gln	10 AGG Arg	330	GCT
30 TCC Ser		AGG		GAC		AGC Ser	230	GGC	280 GAC AGG ASP AFG		MG
AGC		TGC	130	TCC	180	ATC Ile	N	GGC Gly	AAC Asn		MAG
TGG T'rp	80	GGC	13	GGC		GGG G1y		TTC	AAG Lys	320	GCC GGG Ala Gly
20 AGC Ser		CCG		TTC Phe		AGC Ser	220	AGG Arg	270 GGG G1y		GCC
AAA Lys		CCC		GTA Val	170	GAG Glu	22	ACC	GAC		GTC
ASD	70	GAT	120	TCC		GGC Gly		CCC		0	ATT Ile
10 AAA GGG 1 Lys Gly 7		G'rG Val		GTC		TCC		TTC	260 GGA TAC ATC Gly Tyr.Ile	310	TGC ATT Cys Ile
AAAA Lys		CTA		CTC	160	CTC Leu	210	AAG Lys	GGA G1y		TAC
ACT Thr		GAA	110	GGC CTC Gly Leu	16	CTC		TCC	ACG		CGC
CTC Leu	9	CTA	-	ATG Met		AAG Lys		GCT	50 GCG Ala	300	CTC
ACC		GCT		GGC Gly		GAA	200	GAC	250 AAC GCG Asn Ala		GAT, TGC Asp Cys
TTA Leu		GCC	100	GCC	150	TAC	(4	TTC	TTC		GAT. ASP
AAA Lys	20	GCG	7	CGA		TAT TYr		CGC	GGA G1y	90	GAC

FIGURE 2 1/5

			_									
	AGA Arg>	430	TCT Ser>	480	CCG Prov	GCC Ala>		TGT Cys>		CGA Arg>	0	ATT Ile>
380	GAG	4	TTC Phe		TCC	CTT Leu		GCA	620	CGC	670	ATC ATT Ile Ile>
m	AAG		GTC		ATC	0 CTG Leu	570	ACT	9	ATC		GCA
	GAT		ACC	470	AAG ATC Lys Ile	520 GCT CTG CT Ala Leu Le		TCA		CAT ATC CGC CGA His Ile Arg Arg		GCT
370	AIT	420	CTA ACC Leu Thr	4	000 7rg	TCT Ser		N'I'I Ile	, O	AAT Asn	099	GAG
37	AAG Lys		GGC		CAC	GGG	260	TYr YCG TYr Ser	610	GCC AAT Ala Asn		ACT Thr
	AGC-CTC TCC Ser Leu Ser		GGT ATG GGT Gly Met Gly	460	AAA GGT Lys Gly	510 A'NG Met	ניו	I'NT I'YE		TTT TAT GCC GCT Phe Tyr Ala Ala		GCr GGA GGA Ala Gly Gly
	CTC	410	ATG	46	MA	The Ash		CCA AAC Pro Asn		GCC	059	GGA Gly
360		•	$_{\rm G1\gamma}^{\rm GGT}$		GAG	ACA	550	CCA	600	TAT Tyr	v	GC'r Ala
	GM Glu		ACT Thr		ATC Ile	500 ATT Ile	5.	660 61y			•	ATT
	GGT	400	GGA Gly	450	CTC	GCC Ala		ATG Met		TGC Cys	640	CTC ATG ATT Leu Met Ile
350	CTC GGC (Leu Gly (4	GTT' Val		AAT Asn	ኮአፔ ፐሃደ		GGT CTG Gly Leu	290	AAC TAC TGC Asn Tyr Cys	9	CTC
•	CTC		CTA		CAG	490 ATT CCC	540	GGT	U)			GAC
	GAT Asp		GTG	440	GTT Val	45 ATT Ile		TTG		TCC		GCT
340	TCC	390	GGA Gly	4	GGG	TTC	1	GAT Asp	0	GCT ACT Ala Thr	630	GAG
ň	AAT Asn		GCT		GAC	TTT Phe	30	ATC	580	GCT		GGC Gly

FIGURE 2 2/5

720	AGG Arg>	GAT Asp>		TTG Leu>		GGA Gly>	0	GAT Asp>	096	GGG Gly>	ACT Thr>
	CAN Gln	CGT		AGC	860	TTG	910	GCT		GCT	TCC Ser
	GCr TTA TCT Ala Leu Ser	760 AAG GAC Lys Asp	810	GAG	ω			AGG Arg		GAT GCT ASP Ala	1000 GCG ACT Ala Thr
710	TTA			ATG Met		GAA Glu		CCA	950	GAA	10(GCG Nla
•	GCT	GAT Asp		TTG GTT Leu Val	850	ATT ATT GCA GAA Ile Ile Ala Glu	900	GAT CCA A	0,	CTG	CAT
	AGG Arg	750 CCG 1GG Pro Trp	800	Trig	8	ATT 11e		NCT Flyr		AG1' Ser	GCT
700	GCC TGC Ala Cys		ω	GT'A Val				CAT AMG His Met	940	AGC	990 AAT Asn
7(AGG		GGA Gly		CCG	890	CAT	6	GAG Glu	N'r Ile
	GIT	740 AC'T GCC T'CA Tilr Ala Ser	190	GGG GCT Gly Ala	840	GCG Ala	ω.	rat Iyr		ATT Ile	980 GTC AAT TAC Val Asn 1yr
	GGA 171C Gly Phe	740 ACT GCC Thr Ala	75			CGA GGA Arg Gly		GAT GCT		TCT TGC.ATF Ser Cys Ile	980 AAT Asn
069				GAA Glu		CGA Arg	880	GAT Asp	930		g GTC Val
	$_{\rm G1y}^{\rm GGA}$	CAG Gln		GGC	830	AAA Lys	88	rgr Cys		rcc Ser	GAG Glu
	TT. Leu	730 GAC CCT Asp Pro	780	A1G Met	ω	ATG Met		AAT' Asn		GTC Val	70 GAA Glu
680	666 61y			GTG		CAT GCA His Ala		GCA GTC Ala Val	920	GGT Gly	970 CCT GAA Pro Glu
_	CCA ATT O	GAT		TT. Phe	820		870	GCA Ala	O1	CTT	TCA Ser
	CCA	AAT Asn	20	GGT	8	GNA		GGT Gly		$_{\rm G1y}^{\rm GGG}$	GIC Val

FIGURE 2 3/5

	AAG Lys)		CAC His	20	AAG GGA Lys Gly>	1200	CCC GAG Pro Glu>	GAA Glu>		CAC AAC TCA His Asn Ser>		CCA
	TTC Phe	1100	GGA	1150		•	CCC	CAT		AAC	1340	MT
1050	AAG G17 1TC Lys Val Phe	7	ATC Ile		ATr Ile		AAT' Asn	CAN Gln	1290	CAC	13	TCA
	AAG Lys		ATG		ACA	1.190	Tric Phe	1240 CAG CAA Gln Gln		GGC Gly		GGT
	AAG Lys	06	TCG	1140	GCG	=	CZA	MAG Lys		GGA GGC G	0	CTC
1040	AAT GCC ATC AAG Asn Ala Ile Lys	1090	AAG TCG		CTT GAA GCC ATT GCG ACA Leu Glu Ala Ile Ala Thr		TGG.C'T' CAT CCC AGC ATA AAC CAA TTC AAT CCC GAG Trp Leu His Pro Ser Ile Asn Gln Phe Asn Pro Glux	AAG AAG Lys Lys	1280	777C Phe	1330	TTC ICA GCC 1TC AAG CCA IGA TIA CTC GGT TCA AAT Phe Ser Ala Phe Lys Pro
H	GCC		ACT		GCC Ala	000	ΛΊ.Λ Ile	AAC Asn	12	GGA Gly		TGA
	AAT Asn		GCA	1130	GAA	1180	AGC	GCC Ala		'I'TC Plie		CCA
1030	GGG GAT CTT CCC GAG ATA Gly Asp Leu Ala Glu Ile	1080	ATC AAT GCA Ile Asn Ala	7	CTT' Leu		CCC	1230 TTC GAC ACA GTT GCC AAC Phe Asp Thr Val Ala Asn	0	TCA AAT TCA 1TC Ser Asn Ser Phe	1320	MG Lys
10	GAG				GG1' G1y		CAT	ACA Thr	1270	AAT	. "	TTC Phe
	CCC Ala		GAA ATC ACA Glu Ile Thr	20	GGG Gly	1170	.C.r.r Leu	12 GAC ASP		TCA		GCC
	CTT	1070	ATC Ile	1120	TCA			TTC		ATC Ile	1310	T'CA Ser
1020	GAT' Asp	-			CTT GGA GCA TCA GGG Leu Gly Ala Ser Gly		GGC Gly	1210 GTG GAA Val Glu	1260	GTr GCr Arc Val Ala Ile	13	'rrc Phe
	GGG G1y		AAG Lys		GGA Gly	1160	ACC	1210 GTG GZ Val G		Grr Val		GCT
	GCT	09	AAC ACC Asn Thr	1110		Ħ	ACC Thr	TCA Ser		AAT Asn	0	GTT GTA GCT Val Val Ala
10	CTT	1060	AAC Asn		TGT Cys		λ'Γλ Ile	CCA	20	GTG Val	1300	GTT Val

FIGURE 2

CGGAAGAGCG TAATACCGGG ATAGITCCIT GAIAGTFCAI' ITAGGATGTT' 1TACTGCAAI CCCTIGICAA IGGCATIIIAA GATAAGCIIIA TAAMAAAAAA AAAAAAAAAA AAAAACTCGAG TATTIAGAAAG AACGAGGCAA GAITTIGITT CAIGIITTIGTG ITTGTAITTAC ITTCITTITIG GGGGGGCCCG GTACCCAA1T CGCCCTATAG TGAGTCGTAT GACAATTCAC TGTCCGTCGG MAITTGITGC TGAGACAGIG AGCTICAACT IGCAGAGCAA ITTTTTACAT GCCTIGICGT ANTCGANGAT TATTTCCA1TY CTAATCCAGT CTCCGNCGAG 1TTGAGAATC TATCTGTTG

FIGURE 2

Sequence Range: 1 to 2046

09	GGAT	120	STGT	TGG Trp		TCC Ser		TCC Ser		TGC Cys	0.4	GGA Gly
	CCGCTCTAGA ACTAGTGGAT		GGCACGAGTY TYCTTACTYG GGTCGGCTCA GCTCAGGTGT	160 TCC CCT TTC TGT ACG ' Ser Pro Phe Cys Thr '		CGT	0	CTC	310	CCT TO Pro C	360	TTC Phe
20	IGN 1	110	CA	TG	210	CCA	260	ACT Thr		GAT		C'IC Leu
	TCT		נכפכו	160 TTC	0	GAC Asp		agg arg		CTC	o	TCC Ser
			GGTC	CCT		AAC Asn		CGG	300	TGC	350	GC'r Ala
40	3000	100	TTG	TCC Ser	0	SAC	250	CGC	m	CAN		'r'r'c Phe
	ACTAAAGGGA ACAAAAGCTG GAGCTCCACC GCGGTGGCGG		TTAC	150 r GCG l Ala	200	TCC		CGT		TTC		GGA TTC Gly Phe
0	2 (((0	r TTC	GTT Val		TCA		TCC	290	ACC Thr	340	GAT AAC Asp Asn
30	CCAC	90	SAGT	C GCT TCT 1GC ATG G r Ala Ser Cys Met V		CCC ACT Pro Thr	240	CTC	29	TCC		
	NGCT		SCACO	140 r 1'GC c Cys	190	CCC Pro	(1	CGC		GGA		GGG Gly
20	rg g	80	JC G	r TC		ATG Met		CTC		CGC	330	Crrc Leu
	AAGC		SAAT	d dC		TGC	230	CGG Arg	280	CTC	(')	TTC Phe
	ACAA		GCAGGAATTC	Z L	180	GCT GCA Ala Ala	2.	AAG Lys		TCC		CGC
10	GGN .	70	SCT (130 3 GCG t Ala	••	GCT Ala		CAC		TGC	320	CAA
	AAAG		cccceeecr	A ATG Met		GTA Val		TCC	270	CAT His	33	CAG Gln
	ACT		Ö	TCCA	170	CTC	220	CTT		TCC		AAC

FIGURE 3 1/6

£		<i>_</i>		. .							
ACT Thr		GAA Glu		GTG Val		TAC Tyr	009	AAC	TCT		GAC Asp
CGC		CAG	200	GTT GTG Val Val	550	G1T Val	•	GAG AAC Glu Asn	MG		ATG Met
GGC Gly	450	CCT GCA Pro Ala	2(G1'A Val		GAT Asp		AGT.GAG ATA Ser Glu Ile	ATC Ile	069	GAG AGG Glu Arg
400 CTC Leu				CGA Arg		CCC	290	GAG Glu	640 GAG Glu		GAG Glu
GG \rg		CAN		CAA AGG GIn Arg	540	GAC Asp	55	AGT. Ser	GGA G1y		TCC
390 GGC CAC CTG A Gly His Leu A	440	GCT ATG Ala Met	490	CAN	יט	CAT		GGC ATA Gly Ile	630 AGA ATT GCC Arg Ile Ala	680	CCA AAG TTC Pro. Lys Phe
390 CAC His	Ÿ	GCT		ANG Lys		GGC Gly		GGC Gly	630 Arr Ile	39	CCA AAG Pro. Lys
GGC		G'rG Val		ACC	530	CTA Leu	580	AGT Ser	AGA Arg		
CGC		GCT	480	CCT GCT Pro Ala	55	CCT		ATA AGT Ile Ser	ACG		GCC
380 TCA AAT Ser Asn	430	A'rG Met	•	CCT		AC'r Thr		CTA GAC GGA Leu Asp Gly	620 Trr: CCC Phe Pro	019	TGG GTG Trp Val
TCA Ser		G1'C Val		MA		GTG Val	570	GAC	620 Trr CO Phe P		TGG Trp
CGF		GAG	470	ANG	520	GTG Val	٠.	CTA	CAG		GGC
CTT Leu	420	TCC GGG GAG Ser Gly Glu	4	AAT Asn		660 61y		CTC	TC'F Ser	099	GAT
370 CCT Pro	•			ACA Thr		ATG Met	260	AAT	610 TGC Cys	v	ACA Thr
AAG Lys		CAT	•	TCC	510	ggr	56	AAC	GAC		TCC
TCC	410	TCC	460	GTC	υ,	ACA		TAC	Trc	650	TTT Phe

FIGURE 3 2/6

	ΕΩ		⊱ 0		ا Ω	E⊣ O		υQ		< 4
	GAT Asp		1GT Cys	840	GAT Asp	TG'r Cys		GAC Asp		ACA Thr
740	GCA GAT Ala Asp	790	AAG Lys	w	AGC	TYT. Phe		ATG Met	980	TGT GCA Cys Ala
7.	Tra		NGA Arg		TTC Phe	CCC	930	GCA	36	
	GCA		MA	830	GT'A Val	880 AGT Ser	O,	CTT		GCC
	NAA Lys	780	CTC AAT Leu Asn l	Έ	AAG	870 TAT AAG AAG ATC TYF LYS LYS Ile		GCT ATT Ala Ile		ACT
730	AAG	•	CTC		GGT ATG Gly Met	AAG Lys	920	GCT	970	NTN TCA 1
	GGC Gly		GAG		GGT Gly	870 AAG Lys	9	TCC		ATA Ile
	GCA Nla	770	AAA Lys	820	GGC Gly			GGA Gly		TCG
720	ACT	./	ATG Met		TTG	TCA		A'TG Met	096	AAC TAT A
-	CTG		GCG		GGA Gly	860 AGG ACT Arg Thr	910	AST	0.	AAC
	A'I'G Met		GAT ASD	810	TCC	86 AGG Arg		ACA Thr		CCT
710	TAC	760	GAA	~	GGC	CTG		TTT TCT ACC Phe Ser Thr	950	ATG GGC Met Gly
7	ATG CTT' Met Leu		ACT Thr		ATY	GCT	006	TCT	9,	ATG Met
	ATG		ATC	800	CTC	850 GAA G1u	01	TTT Phe		TGG Trp
	TTC Phe	750	GGA G1 <u>Y</u>	ä	GTT Val	ATT Ile		CCT		$_{\rm GGA}^{\rm GGA}$
700	AAG Lys	•	$_{\rm G1\gamma}^{\rm GGT}$		GGA Gly	TCC	068	GTA Val	940	TTG

FIGURE 3

1020 1030	CAC ATA ATC AAA GGC GAA His Ile Ile Lys Gly Glu	1070 1080	GCC GTT TTA CCT GTT Ala Val Leu Pro Val	1120 TCA CAG AGG AAT AAT Ser Gln Arg Asn Asn	1170	AAT CGT GAT GGA TTT ASA AKG ASP Gly Phe	1220	GAG GAG TTA GAG CAT Glu Glu Leu Glu His	1260 1270	GAA 1717 CTA GGT GGG AGT Glu Phe Leu Gly Gly Ser	1310 1320	CCT CAC CCT GAA GGA GCT Pro His Pro Glu Gly Ala
Ä	AAC Asn		GAT GCG Asp Ala	1110 CGA GCT TTG Arg Ala Leu	1160	GAC AGT Asp Ser	1.210	CTT CTT GAG Leu Leu Glu	7	GCG GAA Ala Glu		GAG CCT Glu Pro
1010	GCT GCG Ala Ala	1060	GGC TCG Gly Ser	TGC		TGG	1200	GTT TTA Val Leu	1250	NITT TAT	1300	ATG ACC (Met Thr (
	AAT Asn	1050	TGT GGT Cys Gly	1100 GTA GCA Val Ala	1150	TCG AGA CCA Ser Arg Pro	. 12	GCT GGA Ala Gly		GCA ACC Ala THE	1290	GCC TAC CAC
1000	TGT ATA CTG Cys Ile Leu	Ä	ATG CTT Met Leu	GGT TTC Gly Phe	1140	MA GCT Lys Ala	1190	GAA GGA Glu Gly	1240	AGA GGT Arg Gly	12	GAC
066	AGT AAC TTC Ser Asn Phe	1040	GCA GAC ATG	GGT TTG GGA Gly Leu Gly		GAC CCT ACC Asp Pro Thr	1180	GTG ATG GGA Val Met Gly	1230	GCA AAG AAA Ala Lys Lys	1280	rrc acr rgc Phe Thr Cys
	K W		Ō <	ŏö	1130	ÖZ	118	ÖŽ		ŏ ~		i a

FIGURE 3

TCG Ser		GCT Ala		AAC Asn		CTT	1560	AGG Arg	660 614		GTC Val
GTC		TCC AC'F CCT Ser Thr Pro	20	CAN	1510	CTT CTP Leu Leu	1.5	GCA ATA AGG Ala Ile Arg	GAA		MG Lys
1360 CAG TCC GGA Gln Ser Gly	1410	AC'T Thr	1460	GGC Gly		CAC		GCA		1650	AAA CTG Lys Leu
1360 TCC	Ä			TTC Phe		GGT Gly	09	GTT CAG	1600 GAC CCG GAC Asp Pro Asp	16	MM Lys
CAG		ACT		1GT Cys	1500	A'IC I le	1550	GTT Val			GAG
GCT	00	TAC ATA AAT GCG CAT GCA ACT Tyr Ile Asn Ala His Ala Thr	1.450	CAC	1	ATG		GGC GTA GAA GCA GTT GCA GTA Gly Val Glu Ala Val Ala Val	GAA	0	CCT AAG AAG Pro Lys Lys
1350 AAG GCC TTG (Lys Ala Leu A	1400	CAT		GCC		TCG		GCA	1580 1590 CCA AAT ATT AAT TTG C Pro Asn Ile Asn Leu C	1640	MG
1 GCC Ala		GCG		GCT CTC Ala Leu	0.0	TCC ACC AAA Ser Thr Lys	1540	GTT Val	15 AAT Asn		CCT' Pro
MG		AAT Asn	1440	CNA GC'r Gln Ala	1490	ACC Thr	-	GCA	ATT		GGC Gly
1340 TGC ATA GAG Cys Ile Glu	1390	ATA Ile	1,	CAA		AAT TCC A		GAA Glu	NAAT' Asn	1630	CTC GTC Leu Val
1340 ATA GA Ile G		AAT TAC Asn Tyr		TAC		AAT Asn	1530	GTA	158 CCA Pro	-	CTC
		MT Asn	30	GAA Glu	1480	GTG Val	Ŧ	GGC Gly	CAT		CTG
CTC	1380	GAC GTA Asp Val	1430	AAG Lys	•	AGA Arg		GGT Gly	ATC Ile	1620	AAA Lys
1330 GTG ATC Val Ile	ਜ	GAC		GAT ATC Asp Ile		CTG	0	GGA GCT GGT Gly Ala Gly	1570 GGA TGG ATC Gly Trp Ile	16	GAT GCA AAA CTG Asp Ala Lys Leu
GTG Val		GAA G1u	•	GAT	1470	GAG	1520		GGA Gly		GAT Asp
GGT	1370	AGG	1420	GGA Gly	14	AGT Ser		GGA Gly	ACA Thr	1610	GTG

FIGURE 3 5/6

1680 1690 1700	TCA TTT GGG TTC GGC GGC CAT AAC TCA TCC Ser Phe Gly Phe Gly Gly His Asn Ser Ser	1730 1740 1750 1760	AAC TAG A AAAGAGTCIG TGGAAGCCGA GAGTCTIITGA Asn ***	1790 1800 1810 1820	GAACTCATGC ACGTTAGTAG CTTCTTATGC CTCTGAAAACC GAGATAGACC GGCTACTCGA	1850 1860 1870 1880	GGGGATGCCA AAGATACTCC TTGCCGGTAT TGGTGTTAAG AGATCACTGC 1TGTCCCTTT	1910 1920 1930 1940	TATITICITIC TICITITICAG AGCITTAACC GAGGIAGICG TAITITICGAG CITITICGAAT	1970 1980 1990 2000	ACATGITCGT TAICGGAICA AIGIGITICI ICIAAGAICA ITIGIAATGC AIAITITIGAA	2030 2040	
1670	T'TG TCC AAT Leu Ser Asn	1720	GCC CCC TGC AAC Ala Pro Cys Asn	1780 ·	CGTTAGTAG CTTCT	1840	AGATACTCC TrGCC	1900	rettrigag ageit	1960	ATCGGATCA ATGTG	2020	
1660	ANG GTC GGT Lys Val Gly	1710	ATA CTA TTT Ile Leu Phe	1770	GAACTCATGC A	1830	GGGGATGCCA A	1890	TATTTTCTTC T	1950	ACATGTTCGT T.	2010	

FIGURE 3 6/6

Sequence Range: 1 to 1921

09	CGGCACGAGG TCACCTCTTA CCTCGCCTGC TTCGAGCCCT GCCATGACTA CTACACCTCC	120	GCNTCCTTGT TCGGNTCCAG GCCCATCCGC ACCACCCGCA GGCACCGGAG GCTCANTCGA	180	GCTTCCCCTT CCGGGGGGC ANTGGCTGTG GCTCTGCAAC CTGCACAGGA AGTTACCACA	220 GrG ACT GGA ATG Val Thr Gly Met>		TAC AAT AAT Tyr Asn Asn>	320	rrr GAT TGT Phe Asp Cys>	370	: TCC ACA : Ser Thr>
20	CATGACTA	110	כעככפפעפ	170	GCACAGGA	220 T GrG ACT 1 Val Thr	270	TTC Phe			0 *	CAA TTT CCT ACG AGA A'IT GCT GGA GAG ATC AAG 'IC'I' T'IC 1CC ACA Gln Phe Pro Thr Arg Ile Ala GIY Glu Ile Lys Ser Phe Ser Thr
40	CCCT GC	100	cecy ee	160	CAAC CT	GTA GT Val Va	260	GAT GT Asp Va	310	NTA GA Ile Gl	3.60	ATC AM Ile Ly
	TTCGAG		אככאככ		GCTCTG	210 CGG CGA Arg Arg		GAC CCT Asp Pro		AGT GAG Ser Glu	350	GGA GAG GIY Glu
30	resectes	06	CCATCCGC	150	receiere	200 AAA CAG Lys Gla	250	GGC CAT GAC CCT GAT GTT Gly His Asp Pro Asp Val	300	GGC ATA AGT GAG ATA GAG ACC Gly Ile Ser Glu Ile Glu Thr	m .	ATT GCT
20	crcrra cc	80	ATCCAG GC	140	SGAGGC AA	AAG AAG CCA AGT ATC AAA CAG CGG CGA GTA GTT Lys Lys Pro Ser Ile Lys Gln Arg Arg Val Val		CCT CTA Pro Leu	290	ACG AGT Thr Ser	340	ACG AGA . Thr Arg
10	GG TCAC	70	GT TCGG	.130	TT CCGG	190 AAG CCA Lys Pro	240	GIG ACT Val Thr		GAT GGA Asp Gly		rrr ccr Phe Pro
	CGGCACGA		GCATCCTT		GCTTCCCC	AAG AAG Lys Lys	230	GGT GTG Gly Val	280	CTG CTT Leu Leu	330	GCT CAA Ala Gln

FIGURE 4

420	ATG Met>	ATC Ile>		CTC Leu>		GAA .	0	1TC Phe>	099	TGG Trp>	1Tr! Phe>
	mc	GGA Gly		GTT	260	ATT	610	CCT 1TC Pro Phe		GGA Gly	AAC Asn
	MG	460 AAT GGT Asn Gly	510	GGA Gly	U)	GCC		GT'A Val	-	TTG	0 AGT Ser
410	GAC	46 AAT Asn		TGC		GAT Asp		TGT	029	GAC	700 ACG AC Thr Se
	ANG AGG ATG Lys Arg Met	450 GCA TTA ACA Ala Leu Thr		AAA Lys	550	AAT Asn	009	T'IT Phe	v	GCA ATG (Ala Met)	TGT GCA C
	AGG A	TTA	200	AAA AGA AAA Lys Arg Lys	S.	Tric		ANG ANG ANT CCC Lys Met Asn Pro		GCA	TGT Cys
400	TCC AAG Ser Lys	450 GCA Ala				GT'A Val		ANT	0	CTT	690 GCT Ala
4		MAA		GAT		AAG Lys	290	λ'NG Met	640	ATG Met	AC'F Thr
	CTC	AAG Lys	490	CTA	540	N'rG Met	α,			SCT Ala	TCT Ser
	CCG AAG Pro Lys	440 GCC GGC Ala Gly	4	GAG Glu		GGA G1y		TCA TAT AAG Ser Tyr Lys		GGA TCA Gly Ser	80 ATA Ile
390	CCG			AAA Lys		GCA ATG GGT Ala Met Gly	280	TAT Tyr	630	GGA Gly	o TCG Ser
	GCC Nla	ACT		ATG Met	530	ATG Met	32			ACA AAT ATG Thr Asn Met	
	GTC	430 rg Crg st Leu	480	GTG Val	u,			ATT Ile		AAT' Asn	670 CCC AAC TAC Pro Asn Tyr
380	TGG Trp	žΣ		GAT Asp		TCA	•	AGG Arg	620	ACA Thr	670 CCC N Pro A
	GGT Gly	TAC		GAA	520	GGC Gly	570	CTA	v	ACC	GGC Gly
	GAT. Asp	CTT	470	ACC	52	ATT		GCC Ala		GCT	ATG Met

FIGURE 4 2/6

	GrG Val>		GGA Gly>		ACT Thr>	006	GGG G1y>	AAA Lys>		TGC Cys>		ATT Ile>
	GAT (800	ATC C	850	CCT ACT Pro Thr	9	ATG G Met G	AAG A Lys L		ACT T The C	0	GTG A Val I
750	GCA (8	GGT /		GAC C		G'rr A	SCA A	066	TTC A	1040	GGA G
	GNA		NIT I		GCC (890	TTT (Phe	940 CAT GCA His Ala	•	AGT Ser 1		GCT O
	AGA GGC Arg Gly	190	CCT	840	AAT	æ	GGN Gly	GAG Glu		GGA	0	GGA Gly
740	aga arg	7.5	۸٬۲۸ 11e		nga Arg		GAT Asp	TT.A Leu	980	GGT GGA Gly Gly	1030	GAT Asp
•	ATC Ile		NTC Ile		CAG 31n	880	AAT CGT Asn Arg	930 GAG G1u	o.	CTA		CCT
	AAC CAC ATA Asn His Ile		GT'A Val	830	TTG TCA (Leu Ser (38	AAT Asn	GAG		TYPT Phe		CAC
730	CAC	780	GCG	w	TTG		AGT	CTA	970	GCA GAA Ala Glu	1020	CCT Pro
7			GAT Asp		GCT Nla		GAC Asp	920 CTA CTA Leu Leu	97	GCA	-	GAG Glu
	GCG Ala		TCA	820	CGA Arg	870	TGG Trp	CTA		TAC		ACC Thr
	GCT Ala	170	GGC Gly	8	TCC Cys		CCA	GrG Val		ATT 11e	1010	ATG Met
720	AAT Asn	•	666 61y		GCA Ala		ngn Arg	910 GCT GGA Ala Gly	960	ACT ATF Thr Ile	10	CAC ATG His Met
	CTG		TGC		GTT Val	860	TCA	910 GCT G		GCG		TAC
	ATC Ile	160	CTT	810	TTT Phe	~	GCT	GGA G1y		GGT Gly	00	GCC
710	TGT Cys	7	ATG		GGT Gly		AAA Lys	GAA Glu	950	AGA	1000	GAT

FIGURE 4

1090	GAA GAC Glu Asp>	1140	GAT ATC Asp Ile>	GAG TTA Glu Leu>		GCA GCC Ala Ala>	. 1280	GGG TGG Gly Trp>	1330	GAT ACC Asp Thr>	1380	GTC GGT Val Gly>
	AGG Arg		GGA	1180 CAA AAC AAC Gln Asn Asn	1230	GGA Gly	ä	ACT		CCA GAT GAA GGC GTG Pro Asp Glu Gly Val		AAG Lys
	TC'r Ser	1130	CCA GCT Pro Ala			CTC		AGG Arg		GGC Gly	1370	ATT Ile
1080	GTC Val	ਜ		CAA		CTT	0,	GCA ATA A	1320	GNA	13	Asn Ile
	GGA Gly		ACT Thr	GGC	1220	CAC CTT His Leu	1270	GCA Ala	-	GAT		AGA CTG Arg Leu
	TCA GGA GTC TCT Ser Gly Val Ser	50	TCC	1170 TGT TTC GGC Cys Phe Gly	17	GGT (CAG Gln		CCA	0	nga Arg
1070	CAG Gln	1120	ACA T'hr	TGT Cys		ATT		GTT Val	1310	AAC Asn	1360	GAG Glu
1	GC'r		GCC Ala	CAC	01	TCA ATĠ Ser Met	1260	TCA GTA Ser Val	7	GAN AAC Glu Asn		MAG
	TIG		AAT GCA CAT Asn Ala His	1160 CTT ATC Leu Ile	1210	TCA Ser		TCA		AAT ATT AA'T TTG Asn Ile Asn Leu		GGC CCT AAG Gly Pro Lys
90	AAG GCT Lys Ala	1110	GCA Nla	1] CIT Leu		AAA Lys		GTT Val	00	AA'r Asn	1350	CCT Pro
1060		•		GCT		ACC Thr	1250	GCA Ala	1300	ATT	-	GGC Gly
	GAG Glu		ATA Ile	1150 TAC CAA TYF GIN	1200	TCT	H	GAA		AAT Asn		GTG
	ATA Ile	1100	TAC	1150 TAC CO Tyr G	,	AAT		GTG Val		CCG	1340	CTC
1050	TGC	7	AAT Asn	GAG Glu		GTG Val	01	GGT' Gly	1290	CAT CCG	13	TTG
	CTC		GTA	AAA Lys	1190	AAA Lys	1240	GGT Gly	-	ATC Ile		AAA Lys

FIGURE 4

1390 1400 1410 1420 TTG TCT AAT TCA TTC GGG TTT GGT GGG CAC AAC TCG TCC ATA CTC TTC Leu Ser Asn Ser Phe Gly Phe Gly Gly His Asn Ser Ser Ile Leu Phe> 1480 GCC CCT TAC AAC TAG GGCGTTT CATGTGGGA ATTCTACTCA ATCTATCAAA Ala Pro Tyr Asn ***> 1460 1470 1450 1440 1430

1490	1500	. 1510	1520	1530	1540
GCTGAAGTTT	TGAGGACTCC	GCTGAAGTTT TGAGGACTCC AGCATGTTGG TAGCTCCTTA CGTCTCTAGA CATGCCCATG	TAGCTCCTTA	CGTCTCTAGA	CATGCCCATG
1550	1560	1570	1580	1590	1600
AGTTTTGTGT	CGGGAGCTGT	AGTTTTGIGT CGGGAGCIGT AGTCGGAACC AIGACGGATT GAGIACTCAT GGCGACACAG	ATGACGGATT	GAGTACTCAT	GGCGACACAG
1610	1620	1630	1640	1650	1660
GATATACTCC	TTGCTAGAAT	GATATACTCC TTGCTAGAAT TGTTAGAGCA CTATTCATTA TCCCAFTTTFF TTTCTGAAAT	CTATTCATTA	TCCCATITIF	TITCIGNAAT
1670	1680	1690	1700	1710	1720
CTCCCTCCTT	ACGGTAGTTG	CTCCCTCCTT ACGGTAGTTG TACTTTCGAG CGTTTCATCG AGTCAGTGAA GAAGAGAACA	CGTTTCATCG	AGTCAGTGAA	GNAGNGNACA
1730	1740	1750	1760	1770	1780
AAGCTAACTC	GGGCACGTAG	AAGCTAACTC GGGCACGTAG TAACCATTIG CCCITTGTTY TGCTCTCTAT TTTATCGCCG	CCCTTTGTTT	TGCTCTCTAT	TTTATCGCCG
1790	1800	. 1810	1820	1830	1840
TTTTGTGGGT	TANANTTERGT	TTTTGTGGGT TANANTTFIGT ANAACTAGAC GACTGGTTTG TTTTCFCTFG ATCAFFGGAG	GACTGGTTTG	TTTTCTCTTG	ATCA'I'IGGAG

FIGURE 4 5/6

	٠			1920	1910
NAAAAAAAA	NANNANANA	ATAAAAAAA	TTCATTGATG	NTGINTGGCC ATATTTGCCT TTCATTGATG ATAMAAAAA AAAAAAAAAAAAAAAAAAAAAA	NTGTATGGCC
190(1890	1880	1870	1860	1850

AAAAAAAA AAAAAAAAAA A

FIGURE 4 6/6

09	120	169	217	265	313	361	409	457	505
CTGGTACGCC TGCAGGTACC GGTCCGGAAT 1'CCCGGGTCG ACCCACGCGT CCGTCTTCCC	ACTCCGATCG TICTTCTTCC ACCGCAICTC TTCICTICTC TTGGCITCTC CGCCATCCTC	CGCCGCC ATG CAT TCC CTC CAG TCA CCC TCC CTT CGG GCC TCC CCG CTC Met His Ser Leu Gln Ser Pro Ser Leu Arg Ala Ser Pro Leu 1	GAC CCC TTC CGC CCC AAA TCA TCC ACC GTC CGC CCC CTC CAC CGA GCA Asp Pro Phe Arg Pro Lys Ser Ser Thr Val Arg Pro Leu His Arg Ala 15	TCA ATT CCC AAC GTC CGG GCC GCF TCC CCC ACC GTC TCC GCT CCC AAG Ser lle Pro Asn Val Arg Ala Ala Ser Pro Thr Val Ser Ala Pro Lys 35	CGC GAG ACC GAC CCC AAG AAG CGC GTC GTG ATC ACC GGA ATG GGC CTT Arg Glu Thr Asp Pro Lys Lys Arg Val Val Ile Thr Gly Met Gly Leu 50	GTC TCC GTT TTC GGC TCC GAC GTC GAT GCG TAC TAC GAC AAG CTC CTG Val Ser Val Phe Gly Ser Asp Val Asp Ala Tyr Tyr Asp Lys Leu Leu 75	TCA GGC GAG AGC GGG ATC GGC CCA ATC GAC CGC TTC GAC GCC TCC AAG Ser Gly Glu Ser Gly Ile Gly Pro Ile Asp Arg Phe Asp Ala Ser Lys 80	TTC CCC ACC AGG TTC GGC GGC CAG ATT CGT GGC TTC AAC TCC ATG GGA Phe Pro Thr Arg Phe Gly Gly Gln Ile Arg Gly Phe Asn Ser Met Gly 95	TAC ATT GAC GGC AAA AAC GAC AGG CGG CTT GAT GAT TGC CTT CGC TAC Tyr Ile Asp Gly Lys Asn Asp Arg Arg Leu Asp Asp Cys Leu Arg Tyr 115

FIGURE 5

553	601	649	697	745	793	841	883
() m	(2 ×	L 7	<i>(</i>)	(D)	() (0	5D	
GCC	$\frac{GGG}{G1y}$	CTY	GCC Ala 190	ATG Met	TGC	ATG Met	GGC Gly
GGT Gly	GTT Val	TCT Ser	TAT TYE	CTG Leu 205	TAC	CTT	GGA Gly
CTC Leu 140	CTG	CAA	CCC	GGT Gly	ASII 220	GAT	'rrG Leu
GAT Asp	GTG Val 155	GTT Val	ATC Ile	CTC	TCC	GCT Ala 235	666 61y
GCC	GGA	GGG G1y 170	TTC	GAA Glu	ACT	GAG	A'L'F Ile 250
GAC	GCC	GAC Asp	TTC Phe 185	ATT Ile	GCC	GGT Gly	CCA
GAG	aga Arg	TCT	CCT	GCT Ala 200	TGT Cys	CGT	ATT
CTr Leu 135	GAG	1TC Phe	ACC Thr	CTC Leu	GCA Ala 215	CGC	ATC Ile
TCT Ser	AAG Lys 150	GTC	ATC	CTG	ACT Thr	ATC Ile 230	GCA
AAG Lys	GAC	ACT Thr 165	AAA Lys	GCC	TCC	CAT	GCC GCA A
AAG Lys	ATC Ile	CTG Leu	CGG Arg 180	TCT' Ser	AT'r Ile	AAT	GAG Glu
666 61y	AAG Lys	GGT	CAC His	GGG Gly 195	TCA	GCT	ACT
GCC Ala 130	TCC	GGT Gly	GGT Gly	ATG	TAT Tyr 210	GCT	GGC
GTC Val	CTC Leu 145	ATG Met	AAG Lys	AAC Asn	MC	GCT Ala 225	GGA G1y
ATT Ile	CGC	GGA G1y 160	GAG Glu	ACA Thr	CCA	CAT His	GCT Ala 240
TGC	GAC	ACA Thr	ATC Ile 175	ATT Ile	66C 61y	TTC	ATT

FIGURE 5 2/4

937	985	1033	1081	1129	1176	1224	1272
ACT Thr 270	GAA	CGA	GAT Asp	TCT Ser	GTC Val 350	GCC	AAA Lys
CAG Gln	GG'r G1y 285	AAA Lys	'rct Cys	rcc Ser	GAG	CTC Leu 365	ATC Ile
CCT	ATG	ATG Met 300	AAC	GTC	GAA	GAT	GAT Asp 380
GAC	GTG Val	GCA	ATC Ile 315	GG'r Gly	CCT	666 61y	AAG Lys
GAT Asp	TTT Phe	CAT	GCA	CTC Leu 330	TCA	GCT	ACA Thr
AAC Asn 265	GGr Gly	GAA	GGT Gly	GGT	GTC Val 345	CTA	Asn
AGG Arg	GAT Asp 280	TTG	GGA Gly	GAT	66C 61y	ACT Thr 360	MG
CM	CG1' Arg	AGC Ser 295	17G Leu	GCT Nla	GCT	TCT Ser	Trc Phe 375
'ICT Ser	GAC	GAG Glu	TAT TYF 310	AGG	GAT Asp	ACT	GTT Val
CTG	AAA Lys	CTG	GAG	CCA Pro 325	GNA	GCG	AAG Lys
GCT Ala 260	GA'F Asp	GTG Val	GCA Ala	GAC	CTT Leu 340	CAT	MG
AGG Arg	TGG Trp 275	TTG	ATT	ACT	AGC	GCT Ala 355	ATC Ile
TGC Cys	CCC	GTG Val 290	ATT Ile	ATG	AGT Ser	AAT Asn	GCC Ala 370
GCT	AGG	GGA	CCT Pro 305	CAC	GAG Glu	ATA Ile	AAT
GTG	TCT Ser	GCT	GCA	TAT Tyr 320	ATT	TAC	ATA Ile
TTT Phe 255	GCC	GGT Gly	GGA	GCT	TGC Cys 335	AAT	GAG

FIGURE 5

1320	1368	1416	1464	1512	1569	1629	1689	1
TCT GGA Ser Gly	TGG CTT 1'rp Leu	MC GAC Phe Asp 430	ATC TCG Ile Ser 445	TCG GCT Ser Ala	CCA TGA TTACC CATITCACAA GGCACTTGTC ATTGAGAGTA CGGTTGTTCG Pro 465	TCAAACCCAT 1TAGGATACT GTICTATGTA AAAAAAAGTA AGGATTATCA CT1TCCCTIC	TCCAGTTTGA GAATGAAATT ATKTTTATTF TAAAAAAAA AAAAAAGGGC	
A GCC	3 GGC 3 G1y	GAG	GCG	rrc Phe 460	GTA C	TCA C	א אאא	
T GGA u Gly 395	C ACC	C GTG	r Grr	GCT Ala	GAGA	ATTA	NAAA	
r cm's Leu	A AAC A Asn 410	A TCC Ser	AAT Asn	GTG	ATT	ygg	7.7	
C TGT s Cys	ATA Ile	CCA Pro	Grr	TCA GIC Ser Val	тстс	AGTA	ለነነ"	
A CAC	MG GGA Lys Gly	CCT GAG Pro Glu	GAA Glu 440	TCA	CACT	AAAA	k Typ.	
ATC GGA CAC 1 Ile Gly His C 390	ANO Lys	CCT	CAC	AAC Asn 455	SS ×	Ą	r at	
3 ATC 390	ATT Ile	ANT	CAA	CAC	כאכע	ATGT	WAAT	
AAG TCA ATG Lys Ser Met	Thr 405	TTC Phe	CAG Gln	66C 61y	4TTT(PFCT	WTG/	Ę
Ser	GCG	CAA Gln 420	AAG Lys	GGA	ပ ဥ	T. G	is G	, ,
, AAG Lys	ATA	AAT Asn	AAG Lys 435	mc	TTA	SATAG	TTT	ָּרֶבְיּבְיִבְּיִבְּיִבְּיִבְּיִבְּיִבְּיִבְ
ACT	GCT	AlT	AAC Asn	GGA G1y 450	TGA	TAGG	CCAG	מיט מיט מיט מיט
GCA Ala 385	GAA	AGC	GCC	T'IT Phe	CCA Pro 465	AT 1	TC T	#30
AAT	CTT Leu 400	CCC Pro	GTT Val	TCA	AAG Lys	ACCC	TAATCCTGTC	ָרָבָּי בּיַבָּי
ATT	GGT Gly	CAT His 415	ACT Thr	AAT Asn	TTC	TCAA	'FAAT	ָּ֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖

FIGURE 5

Sequence Range: 1 to 1802

. ပ္ပ	1°CC Se r									
CTCC	OCCT:			210	CGT Arg		CGG		GTC Val	CTA
I"FA'F	11 rcc ser	160	TCC	••	ATC Ile		MG Lys		GAC	350 ATC AGC Ile Ser
r S	CAC		CCC		GTC		AAG Lys	300	TCC	35 ATC Ile
ľGCC	CTC C		TCC	00	CCC Pro	250	CCC Pro		GGC G1y	GGC
TCT	IOO ICC Ser I	150	AAT Asn	7(CTC		GAC		TTC	AGC
CATT	SAN 3	•••	CTC		AGC		TCC	90	GTC Val	340 GAG Glu
VI"I"	NIG 0 Jet 0		CGC		GCC	240	GAG Glu	25	TCC	66C 61y
C VC	U OU	10	TTC	190	CGC				GTC	'rcc Ser
CGAC	30000	ř	CCC				MAG		CTC	330 G Crc u Leu
ITTC	SOCO		GAG		CTC	30	CCC Pro	280	GGC Gly	r. C. S.
3G C'	کن دو دو		CTC	180	CCC	2.	GCC		NTG Met	MG Lys
rccg	CGTT	130	CCT	••			TCC		GGC	320 TAC GAC TYr ASP
CGCG	CCGT	٠	TCC		CTC		GCC	270	ACC Thr	TAC TYF
CCN	70 2CG		CCC	20	GCT	220	ACC Thr	•	ATC	TAC
CGAC	rccr	120.	CGC	÷			GCC		GTC	GCC
GGT	CGC	- ·	CTC		GCC		GCT	260	G1'C Val	310 GAC ASP
	הפסירכינאנים כפכסירכיפפס כיודיויכסאככ אכאירויכאידי זיכויויפכסירכ זייויאיריויכוייכ	GGTCGACCCA CGCGTCCGGG CTTTCGACC ACATTTCATT TCTTGCCTCG TTATCTCCGC 70 80 90 100 100 110 CGCTCCTCCG CCGTCGTTCG CCGCCGCCGC C ATG CAA TCC CTC CAC TCC CCT TCC Met Gln Ser Leu His Ser Pro Ser	CATT TCTTGCCTCG 100 CAA TCC CTC CAC Gln Ser Leu His	CATT TCTTGCCTCG 100 CAA TCC CTC CAC Gln Ser Leu His 150 CTC AAT TCC CCC Leu Asn Ser Pro	GACCCA CGCGTCCGGG CTTTCCGACC ACATTCATT TCTTGCCTCG 70 80 90 100 100 CCTCGG CGGTCGTTCG CGCCGCGC C ATG CAA TCC CTC CAC Met Gln Ser Leu His 20 130 140 150 150 Arg Pro Ser Pro Leu Glu Pro Phe Arg Leu Asn Ser Pro 170 180 190 200	GACCCA CGCCTCCGGG CTTTCCGACC ACATTTCATT TCTTGCCTCG 70 80 90 100 100 100 140 140 150 150 170 180 190 190 200 200 300 300 300 300 300 3	TGACCCA CGCGTCCGGG CTTTCCGACC ACATTTCATT TCTTGCCTCG 70 80 90 100 100 140 150 150 150 170 180 190 200 GCC CCT CTC GAG CCC TTC CGC CTC AAT TCC CCC AAG CCC TTC CGC CTC AAT TCC CCC AAG Deu Asn Ser Pro Leu Glu Pro Phe Arg Leu Asn Ser Pro CCC CTC CTC CGT CGC CTC CT	TGACCCA CGCGTCCGGG CTTTCCGACC ACATTTCATT TCTTGCCTCG TO 80 90 100 100 100 100 100 100 100 100 100	GCTCCACCCA CGCGTCCGGG CTTTCCGACC ACATTCATT TCTTGCCTCG GCTCCTCCGG CCGCCGCGCGC C ATG CAA TCC CTC CAC Met Gln Ser Leu His 120 TC GG CCC TCC CCT CTC GAG CCC TTC CGC CTC AAT TCC CCC eu Arg Pro Ser Pro Leu Glu Pro Phe Arg Leu Asn Ser Pro 170 180 190 200 CC GCC GCT CTC CTC CTC CGT CGC CTC AAT TCC CCC TC GC CCT CT CTC GAG CCC TTC CGC CTC AAT TCC CCC TC GC CCT CT CTC CGC CCC TTC CGC CTC AAT TCC CCC TA Ala Ala Ala Leu Arg Pro Leu Arg Arg Ala Ser Leu Pro Val 220 220 230 270 270 280 290 300	GCTCGACCCA CGCGTCCGGG CTTTTCCGACC ACATTTCATT TCTTTGCTTCG 70 GCTCCTCGG CCGCCGCCGC C ANG CAA TCC CTC CAC Met Gln Ser Leu His 120 TC CGC CCT TC CAG CCC TTC CGC CTC AAT TCC CCC eu Arg Pro Ser Pro Leu Glu Pro Phe Arg Leu Asn Ser Pro 170 180 190 200 210 220 230 240 250 270 280 290 300 290 300 210 270 280 290 300 210 270 280 280 290 300 200 200 200 200 200 20

FIGURE 6 1/5

400	GGC CAG Gly Gln	450	GAC CGG Asp Arg		ANG GCT Lys Nla		GAT AAG ASP Lys	0 ACT GTC Thr Val	640	AAG ATC Lys Ile	069	GCG CTG Ala Leu
•	GCC		AAC		MAG	540	ATT Ile	590 CTA ACT Leu Thr		CGG Arg		TCT
	Tric	440	AAG Lys	490	GGC Gly		AAG Lys	GGC Gly		CAC	0	GGG
390	AGG Arg	4	GGC		GCC		TCC	GGT Gly	630	GGT	680	ATG Met
()	ACC		GAC		GTC	0	TCC CTC Ser Leu	580 ATG Met	Φ	AAA GGT Lys Gly		ACA AAC ATG GGG Thr Asn Met Gly
	CCC		ATC Ile	480	λ'ΓΤ Ile	530	7CC Ser	GGT' Gly		GAG		ACA Thr
380	AAA 14TC Lys Phe	430	TYC	4	TGC N'TT Cys Ile		CM		0	ATC 11e	670	ATT Ile
ñ			GGC Gly		TAC		66C 61y	570 G'TT GGA ACC Val Gly Thr	620	CTC		GCC
	TCC		ACG Thr	470	CGC	520	GCC Ala	g'm Val		AAT Asn		TAT Tyr
	GAC GCT Asp Ala	420	GCG Ala	47	CTC		CTC	CTA Leu		CAG	099	CCA Pro
370		7	AAC		TGC		GAT	50 GTG Val	610	GTr	9	ATT' Ile
	T77C Phe		TTC Phe		GAT Asp	510	GCC Ala	560 GGA GTG Gly Val		666 G1y		TTC Phe
	CGC	410	GGC Gly	460	GAC	u,	GAC	GCC		GAC	Q	CCG 1TT Pro Phe
360	GAC	4.]	CGT Arg	•	CTC		GAA	AGG	009	TCT Ser	650	CCG
	ATC Ile		ATC Ile		CGG	200	CTC	550 GAG G1u	9	TTC		'rcc Ser

FIGURE 6 2/5

	TCA ACT Ser Thr		ATC	GCG		TCT	930	GAC		GAG G1 u		TAT
	1CA Ser		GCC AAT CAT Ala Asn His	830 G GCT u Ala	880	'ITA Leu	O	MAG		N'IG Met		
	ATT	780	AAT' Asn	676 G10		GCT		GAT Asp		G'I'T Val	1020	GCA Ala
730	TCG ATT Ser Ile	•	GCC	ACT Thr		AGG	920	TGG Trp	970	177G Leu	10	ATT Ile
			GCC	820 GGA GGA ACT GAG GCT Gly Gly Thr Glu Ala	870	TGC	92			GTA 117G Val Leu		Aïr Ile
	CCA AAC TAF Pro Asn Tyr	770	GCT	820 GGA G1y	ω	GCC		AGG Arg		GGA G1y	0	CCG AIT ATT GCA GAA Pro Ile Ile Ala Glu
720	CCA	7.	TAT Tyr	GCT		GTT Val		TCA Ser	096	GCT	1010	GCG
•	660 61y		1TT Phe	ATT Ile	860	TTC	910	GCC	ov	GGG Gly		GGA Gly
	A1'G Met		TGC	810 CTG ATG Leu Met	36	GGA G1y		GAT CCT CAG ACT Asp Pro Gln Thr		GNA		
710	CIG	760	T'AC T'Y F	CTG		GGA Gly		CAG	950	ATG GGT Met Gly	1000	MA Lys
7	GG'I' Gly		AAC	GAC Asp		TTA Leu	006	CC'l' Pro	36	ATG	-	A'rG Met
	TTG		Ser	800 GAG GCT Glu Ala	850	GGT' Gly	01	GA'F Asp		GTG		GCA ATG AAA CGG Ala Met Lys Arg
	GA'F Asp	750	ACT Thr	8(GAG G1u		ATT		AGG AAT GAT Arg Asn Asp		Trrr Phe	066	CAT
700	ATC Ile	•	GCT	GGT Gly		CCA	890	AA'T Asn	940	GGC Gly	o,	GAG
	GCC Nla		TGT Cys	CGA	840	ATT Ile	8		,	GAT		TTG
	CTT	740	GCA	790 CGC Arg	ω	GTC Val		CAA Gln		CGT	980	AGC

FIGURE 6 3/5

AGG		GAT Asp	1170	ACT Thr		G17' Val		ATC Ile	AYFT Ile		AAT' Asn
1070 GAT CCA /	1120	CTC GAA GAT Leu Glu Asp	11	GTC AAT TAC ATA AAT GCT CAT GCG ACT Val Asn Tyr Ile Asn Ala His Ala Thr		GAG ATA AAT GCC ATT AAG AAA Glu Ile Asn Ala Ile Lys Lys		AAG TCA ATG Lys Ser Met	1280 1310 CTT GGA GCT CTT GAA GCC ATC GCA ACC ATT Leu Gly Ala Ser Gly Gly Leu Glu Ala Ile Ala Thr Ile	1360	ATA ACC ACC GGC TGG CTT CAT, CCC AGC ATT AAT CAA TTT AAT ITE The The The The Gly Trp Leu His Pro Ser Ile Asn Gln Phe Asn
10' GAT ASP	••			CAT		AAG Lys	1260	TCA	1310 GCA AC Ala TI	-	CAA
1050 AAC TGT GAT GCT TAT CAT ATG ACT Asn Cys Asp Ala Tyr His Met Thr		CTr GGT GTC TCC TCG TGC ATT GAG AGC AGT Leu Gly Val Ser Ser Cys Ile Glu Ser Ser	20	GCT	1210	N'M' Ile	12		ATC Ile		AAT! Asn
ATG	1110	AGC	1160	AAT Asn	7	GCC		ACT Thr	GCC	1350	MIT Ile
1060 CAT His	-	GAG		ATA Ile		AA'f Asn	0.0	GAN NTC AAA ATC AAT GCA ACT Glu Ile Lys Ile Asn Ala Thr	1300 r GAA u Glu	#	AGC
ገለፐ ገን r		ATT Ile		TAC	1200	ATA Ile	1250	AAT	C'I'F Leu		CCC Pro
GCT	00	TGC Cys	1150	AAT Asn	1	GAG		ATC	GG'F G1y	0	CA'r His
050 GAT Asp	1100	TCG	•	GTC Val		GCC		AAA Lys	1290 CA GGA er Gly	1340	Cirr
1 TGT Cys		TCC		GAG	06	GAT CTT (1240	ATC Ile	12 TCA Ser	•	TGG Trp
MC		GTC Val	1140	GAA G1.u	1190	GAT Asp	-	GAA Glu	GCA		GGC
1040 GGT GCA GTC A	1090	GGT Gly	ਜ	TCA CCT GAA GAG Ser Pro Glu Glu		GGG Gly		ACC AAG Thr Lys	GGA GGA G1y	1330	ACC
10 GCΛ Λla						SCT	1230	ACC Thr	1280 CTT GC Leu G]	_	ACC
GGT Gly		GCT GAT GGG Ala Asp Gly	30	GTC	1180	CTT' (12	AAC Asn	TGT		ATA Ile
GGA Gly	1080	GAT Asp	1130	$\begin{array}{c} GGG \\ G1y \end{array}$		ACT		AAG Lys	CAC	1320	GGA
1030 17G Leu	Ĥ	GCT' Ala		GCC		TCT Ser	1220	TTC Phe	1270 GGA CAC Gly His	13	AAG GGA 7 Lys Gly 1

FIGURE 6

1410	CAG CAA GIn GIn		GGG CAC Gly His	1510	TITGGTICA	157	'NAA'FGCCT	163	AGCCATTTA	169(CTCTGATITA	175	TTATTTAM		1.
1400	GTG GAC TTC AAC ACT GTT GCC AAC AAA AAG CAG CAA Val Asp Phe Asn Thr Val Ala Asn Lys Lys Gln Gln	1.450	GGA TTT GGA GGG Gly Phe Gly Gly	1500	AAG CCA TGA AITCT ACTTGGTTCA Lys Pro ***	1560	AAATGCACAC CAGTTGCTGA GATAGGGCTT CAACTTGCAG AGCAATTTTT 1AAATGCCT	1620	GTCCTTYGAT AGTTCCTCGA AGCCATTTA	1680	GATGATGITT TACTGIVATA ATCGAAGATG AITCCCATTT TAAATCTAGT CTCTGATITA	1740	TGTATTAGAA AGACCAATGA AAGATTITGT GTCATGITTG IGTTGTCAAT GITATTTAA(1800	ATAMAGCAMA AMAMAMAM MAGGGGGGC GCTCTAGAGG ATCCAGCTTA C'I'
1390	AAC ACT GTT GCC Asn Thr Val Ala	1440	AAT TCT TTT GGA Asn Ser Phe Gly	1490		1550	CAACTTGCAG	1610		1670	ATTCCCATTT	1730	GTCATGITTG	1790	GCTCTAGAGG
	AC TTC AAC sp Phe Asn	1430	GC'r ATC TCG Ala Ile Ser	1480	GCA TYC TCA GCT TYC Ala Phe Ser Ala Phe	1540	GATAGGGCTT	1600	GANTAGGTCG	1660	ATCGNAGATG	, 1720	AAGATTTTGT	1780	MGGGCGGCC
1380	A TCG GTG G o Ser Val A		G'rc Val	1470	GTG	1530	CAGTTGCTGA	1590	GTCGGNAGAG CGTNATACCG GAATAGGTCG	1650	TACTGTAATA	1710	AGACCAATGA	1770	MANAMANA
1370	CCC GAG CCA TCG Pro Glu Pro Ser	1420	CNT GAA GTG AAC His Glu Val Asn	1460	AAC TCG GTT Asn Ser Val	1520	NAATGCACAC	1580	GTCGGAAGAG	1640	GATGATGTTT	1700	TGTATTAGAA	1760	NTANAGCANA

FIGURE 6 5/5

Sequence Range: 1 to 2369

09	CATAMAGAG	120	TTACCATACC	180	ATCCTTTTCT	230 GCC TCT TCC Ala Ser Ser>	280	ATG TCT Met Ser>	.330	TCT CCT Ser Pro>		CCA CTA Pro Leu>
20	כעכפכפוגכפ	110	CTTCGA1TCA	170	CCCAAAGGGT		270	SCC GCC TGC	320	NCC ATC TCC Ser Ile Ser	370	MA TGC GCC
40	CGGGTCGACC	100	CTCCTTTCAT	160	GGTCTTTCAT	220 CCTCCA ATG CCT GCC Met Pro Ala		ACG TGG CTC CTr GCC GCC TGC Thr Trp Leu Leu Ala Ala Cys	310	CTT CCG CCT TCC ATC TCC Leu Pro Pro Ser Ile Ser	360	rr CTC TCC (
30	CCGGAATTCC	06	יופכפפככאככ	150	GCCITTTCCG	210 CAGTCAGTTC	260	C TGT ACG TO U Cys Thr T	0.4	GAC CCT Asp Pro	350	CGC CGG AT
20	GTACGCCIIGC AGGI'ACCGGI' CCGGAAITCC CGGGI'CGACC CACGCGI'CCG CATAAAAGAG	80	AGAGAGAGG ATCCATCGAA TGCGGCCACC CTCCTTTCAT CTTCGAITCA TTACCATACC	140	ATICCGCIGA TCCAITITCC GCCITTICCG GGTCITTCAT CCCAAAGGGT ATCCITTTCT	200 CTCAAAGGGT	250	TCC CCT CTC 1GT Ser Pro Leu Cys	300	CAC CCC TCC His Pro Ser	340	CTC TCC CGC Leu Ser Arg
10	GTACGCCTGC	70	AGAGAGAGG	130	ATTCCGCTGA	190 ATCCTATCTT	240	CTG CTC GCT Leu Leu Ala	290	ACC TCC TTC CAC Thr Ser Phe His	'n	CGC CGA CGC CTC TCC CGC CGC ATT CTC TCC CAA TGC GCC CCA CTA Arg Arg Arg Arg Arg Ile Leu Ser Gln Cys Ala Pro Leu

FIGURE 7

	GTC Val>	TCC Ser>	0.	CGG Arg>	570	CTG Leu>		CAG Gln>		CAT His>	ATA Ile>
	CTC	470 TAT ACA TYE THE	520	CAC		GCT		AAA Lys		GGC G1y	10 GGC G1y
420	ACC			AGG Arg		GTG	610	AGT ATC Ser Ile	099	CTA	AGT Ser
	CAT	TAC		CGC	260	GCC	9	AGT		CCT' Pro	ACG Thr
	TT'C Phe	50 GAC Asp	510	ACC Thr	U,	ATG		CCA		\CT Fhr	GGA GIY
410	TCC AGT' 1 Ser Ser B	460 CAT GAC		ACC ACC Thr Thr		GCA		AAG CCA Lys Pro	650	GTG	700 GAT GGA 1 ASP Gly 1
•	TCC	'IGC Cys		CGC	550	GAG	009	MG		GTG GTG /	CTT
	GGA Gly	CCC	200	CCC ATr Pro Ile	5.	AGG Arg		AAG Lys		GGT Gly	CrG
400	CGC	450 GAG Glu	υ,	CCC Pro		írcc Ser		GTT ACC ACA Val Thr Thr	0	GGA ATG Gly Met	690 AAT Asn
4(CYC	'rrc Phe		AGA Arg	,	CC'I' 'TCC Pro Ser	290	ACC	640	GGA Gly	AAT' Asn
	GCC	TGC Cys	490	TCC	540	rcc Ser	ហ	GTT Val		AC'F Thr	TAC
	TCC Ser	40 GCC Ala	45	GGA G1y		GCT Ala		GAA		GTG Val	680 Trc Phe
390	TCC			TTC Phe		CGA Arg	0	CAG Gln	630	GTT Val	680 GTT TTC Val Phe
	GCT Ala	TAC		TTG	530	AAT Asn	580	GNA		GTA Val	GAT Asp
	TCT Ser	430 C TCT r Ser	480	TCC	и) .	CTC		CCT Pro		CGA	
380	CCT	A3 ACC Thr		GCA		AGG Arg		CAA	620	CGG	670 GAC CCT ASP Pro

FIGURE 7 2/7

	. ^	_	4		^		^	^		. ^		^
0	GC'r Ala>	810	CTC Leu>		AAG Lys>		CT'A Leu>	ATG Met>	0	MG Lys>	1050	GCT Ala>
160	ATT Ile		MG Lys		GGC		Ju Ju	15 S	1000	AAG AAG Lys Lys>	Ä	TCA (
			ر د ت		ÖÖ	_	00	950 ' GG/ ' G1)		23		
	AGA Arg		CCC	850	GCT	006	AAA GAG Lys Glu	950 GGT GGA Gly Gly		T'AT T'y r		GGA Gly
	CCT ACG Pro Thr	800	GCC CCG Ala Pro	α	ACC Thr		ATG Met	ATG Met		TCA	1040	ATG Met
750			TGG GTG Trp Val		CTG		G'rG Val	10 GCA Nla	990	ATT TCA Ile Ser	10	AAT Asn
	'I'I'T Phe		7GG Trp		ATG Met	890	GAA GAT GTG Glu Asp Val	940 TCA GCA Ser Ala		AGG Arg		ACA Thr
	CAA	790	GGT Gly	840	TAC	_		GGC Gly		GAA GCC C'FA Glu Ala Leu	00	TTC GCT ACC Phe Ala Thr
740	, GCT' Ala	7	GAT Asp		CTA		ACC Thr	ATY! Ile	980	GCC	1030	GCT
	rgr		ACA Thr		Trc Arg Phe Met	880	GGA ATC ACC Gly Ile Thr	930 CTC Leu	0,	GM		
	GAT' Asp		TCC	830	Trrc	Ö	GGA Gly	GTT Val		ATT Ile		CCT Pro
730	T'r'r Phe	780	TT'C Phe	•	AAG Lys		GG'r Gly	GGA Gly	970	GAT GCC ATT Asp Ala Ile	1020	GTA Val
7	Thr		TCT		GAC		GAT' Asp	920 TGC Cys	6			11T TGT GTA Phe Cys Val
	GAG		AAG Lys	820	AGG ATG Arg Met	870	ACA Thr	AAA Lys		MT Asn		
	GAG ATA Glu Ile	770	GAG ATC Glu ile	ω			Try Leu	nga Arg		Trrc Phe	1010	CCC Pro
720					AAG Lys		GCA Ala	910 GAT AAA ASP LYS	960	GTA Val	10	AAT
	AGC		GGA Gly		TCT	860	AAA Lys	91 GAT ASP		AAG		A1G Met

FIGURE 7

	TCT Ser>		CAT His>	GGC TCA GAT GCG Gly Ser Asp Ala>	0	TTG Leu>	1290	AGT Ser>		CTA Leu>	
	ata Ile		ASC	1190 SA GAT SE ASP	1240	GCT TTG Ala Leu		GAC AGT Asp Ser		CTA	
06	TCG Ser	1140	GC'r GCG AAC Ala Ala Asn	113 TCA Ser		CGA Arg		TGG Trp	0.0	GTG CTA CTA CTA Val Leu Leu Leu	1380
1090	AAC TAC TCG ATA Asn Tyr Ser Ile	•	GCT			TGC	1280	AGA CCA TGG Arg Pro Trp	1330	GTG Val	
	AAC		ASn Asn	1180 TGC GGG Cys Gly	1230	GCA Ala	13			GGA Gly	
	CCC	1130	ATA ATG AAT Ile Met Asn	1180 TGC GC Cys G	-	GTT GCA TGC Val Ala Cys		TCA		GCT	1370
1.080	ATG GGG WEL Gly	Ξ		CTT Leu		'I'T'T Phe	0,	AAA GCT TCA Lys Ala Ser	1320	GAA GGA GCT Glu Gly Ala	13
•••	ATG Met		TGT' Cys	ATG Met	1220	GGT Gly	1270		-		
	GGA 1'GG Gly Trp	50	AAC 1777 Asn Phe	1170 GCA GAT GTG Ala Asp Val	77	ATC ATA CCT ATT GG'R ATG GGA GG'R 'TTT Ile Ile Pro Ile Gly Met Gly Gly Phe		TCC GAC CCF ACT Ser Asp Pro Thr		GTT ATG GGG Val Met Gly	0.0
1070	GGA Gly	1120	MAC	GAT Asp		ATG Met		CC'F Pro	1310	ATG Met	.1360
ñ	176 Leu		AG'I' Ser	GCA	01	$_{\rm GG'F}^{\rm GG'F}$	1260	GAC	ä	GTT Val	
	GAC		GCA ACG Ala Thr	160 GAA Glu	1210	ATT Ile		1°CC Ser		1'I'T Phe	
09	GCA ATG Ala Met	1110	GCA	1160 GGC GAA Gly Glu		CCT Pro		CAG AGA AAT Gln Arg Asn	00	GAT GGA Asp Gly	1350
1060		•	1'GT Cys	AGA Arg		ATA Ile	1250	AGA Arg	1300	GAT Asp	-
	CTT		GCT	1150 ' ATA ATC Ile Ile	1200	ATC Ile	13	CAG Gln		CGT	
	A'I'G Met	1100	ACT Thr	115 ATA Ile	•	GTA		TCC		AAT Asn	1340

FIGURE 7

GAG GAG TTG GAG CAT GCA AAG AAA AGA. GGT GCG ACT ATT TAC GCA GAA Glu Glu Leu Glu His Ala Lys Lys Arg Gly Ala Thr Ile Tyr Ala Glu>

^		^		^		•		^	^		
CCT Pro>	30	GCT Ala	1530	GCC Ala>		CAC His>		ATG Met>	Grh Val>	0	Syl
30 GAG Glu	1480	TTG GCT Leu Ala>	•	CAT		ATC Ile		TCA ATG Ser Met>	70 TCA Ser	1720	TTC
ACC Trhr				GCC	0	CTT	1620	AMA	16 GTT Val		NAT Asn
ATG		AAG	1520	Asn	1570	GCT	-	ACC	SCA		MTT.
O CAC His	1470	GAG	15	ATA		CAA GCT CTT Gln Ala Leu		Ser	GAA	1710	AAT' ASh
142 TAC TYF	+	ATA Ile		TYC			1610	AAT	166 GTG Val	7	CCG
1400 1410 1420 1430 GGG AGT TYC ACT TGC GAY GCC TAC CAC ATG ACC GAG Gly Ser Phe Thr Cys Asp Ala Tyr His Met Thr Glu		GCT GGA GTG ATT CTC TGC ATA GAG AAG GCT Ala Gly Val Ile Leu Cys Ile Glu Lys Ala	0	TCT AGG GAA GAC GTA AAT 1'AC ATA AA'F GCC Ser Arg Glu Asp Val Asn Tyr Ile Asn Ala	1560	ANA GAG TAC Lys Glu Tyr	16	GAG TTA AAA GTT AAT TCA ACC AAA Glu Leu Lys Val Asn Ser Thr Lys	1640 1650 1650 CTT CTC GGA GCA GCA GTA TCA GTA Leu Leu Gly Ala Ala Gly Gly Val Glu Ala Val Ser Val		CAT
GA'F Asp	1460	Crc	1510	GTA Val	-	ANA		AAA Lys	GGT Gly	1700	ATC
410 TGC Cys	14	A1'r Ile		GAC		GGA GAT ATC Gly Asp Ile	0	TTA	650 GCC Ala	17	TGG
ACT Thr		GTG Val		GAA	1550	GAT	1600	GAG Glu	l GCA Ala		GGG
Tric	0	GGA G1y	1500	AGG	15	GGA Gly		AGA Arg	GGA G1y	0	ACT
100 AGF Ser	1450	GCT Ala	7	TCT Ser		GCr		AAC	40 CTC Leu	1690	AGG
14 GGG Gly		GGA Gly		TCA GGA GTC Ser Gly Val	0	ACT CCG (Thr Pro)	1590	CAA AAC AGA Gln Asn Arg	16 CTT Leu		ATA Ile
3GT 31y		GAT Asp	1490	GGA Gly	1540	ACT	7	GGC	CAC		GCA
CTA CTA Leu	1440	CCT	14	TCA		TCC		TYC Phe	30 GGT Gly	1680	CAG
1390 TTT CTA (Phe Leu (•1	CAC		CAG		ACA	1580	TGT Cys	1630 ATT GGT CAC Ile Gly His	1	GIT CAG GCA ATA AGG ACT GGG TGG ATC CAT CCG AAT ATT AAT TTG GAA Val Gln Ala Ile Arg Thr Gly Trp Ile His Pro Asn Ile Asn Leu Glu>

FIGURE 7 5/7

1770	GGT CCT ANG ANG Gly Pro Lys Lys>		3 111 GGr 7 Phe Gly>	1870	CAC AAC TCG TCC ATA CTC TMC GCC CCT TAC ATC TAG GAC GTTTCCGTGT His Asn Ser Ser Ile Leu Phe Ala Pro Tyr Ile ***>	1930	GTTGGTAGCT	1990	GNACCATGAC	2050	GTAGAGCAAT	2110	GTTGTACTTT	2170	CACGTAGTAA
1760	GTG Val	1810	YCA 1717 GGG Ser Phe Gly	1860	ATC TAG GAG Ile ***>	1920	ACTCCAGCAT	1980	GCTTTAGTCG	2040	CACTTGATAT ACTCCTTGCT AGAATTGTTG GTAGAGCAAT	2100	CCTTGCAATA GTTGTACTTT	2160	TTAACTCGGG
1750	NA TTG CTC	1800	GGT TTG TCT AAT TCA	1850	SCC CCT TAC	1910	AGTTTTGAGG	1970	TGTGTCCGGA	2030	ACTCC1TGCT	2090	ANATCTCCCT	2150	MCAMGCTG
0*	G GAT ACA 1 1 ASP Thr 1	1790	Grc	1840	A CTC TYC C	1900	TCAAAGCTGA	1960	CCATGAGTTT	2020	CACTTGATAT	2080	TTTTCTCTG	2140	IGMGAAGAG
1740	CCA GAT GAA GGC GTG GAT ACA AAA TTG Pro Asp Glu Gly Val Asp Thr Lys Leu	1780	CTG AAC GTT AAG Leu Asn Val Lys	1830	TCG TCC AT	1890	GTGGAATICT ACTCAACATA TCAAAGCIGA AGTTITGAGG ACICCAGCAI GTIGGTAGCT	1950	CCTTACGICT CTAGACATGC CCATGAGTTT 18TGTCCGGA GCTTTAGTCG GAACCATGAC	2010	GGATTGAGTA CTCATGGCGA	2070	TCATATTTTT TTTTTCTCTG ANATCTCCCT	2130	CGAGCTITIC ATCGAGTCAG IBAAGAAGAG AACAAAGCIG TIAACIICGGG CACGIIAGTAA
1730	AAC CCA GAY Asn Pro Ast	H	GAG AGA CTC Glu Arg Let	1820	GGG CAC AAC Gly His Asr	1880	GTGGAATTCT	1940	CCTTACGICT	2000	GGATTGAGTA	2060	ATTCATTATC	2120	CGAGCTTTTC

FIGURE 7 6/7

				CTCTAGAGG	2360 AGGGCGGCCG CTCTAGAGG
NAAAAAAAA	NANNANAANN	AAAAAAAAA	ANNANNANAN	TGGNAATBAA AAAAAAAA AAAAAAAA AAAAAAAAA AAAAAAAA	TGGAAATAAA
2350	2340	2330	2320	2310	2300
ATGTATGTTT	TAATTGGGGR	TYCTICATTGA	Trecritical	MCTAGNAGA CTGGTTTAGA TTGGTTTGTT TYCTCATTGA TAATTGGGGR ATGTATGTTT	NACTAGNAGA
2290	2280	2270	2260	2250	2240
AAATTTIGTAA	TGTGGTTTTA	NICACCGTIT	TCTCTATITC	CCATTIGCCC 111161TT16C 1CTCIATITC AFCACCGT11 1GIGGTITTA AAATT11GTAA	CCATTTGCCC
2230	2220	2210	2200	2190	2180

FIGURE 7

Sequence Range: 1 to 2374

09	CACACCAAAC	120	ACAGACAGAC	180	TCTTCGNTTC	240	TCCCAAAGGG	300	ccrecceccr	360	TCTACCTCCT	420	creaceace	480	CGCGGATCCA
20	-A-CNTGGTC CGGNATTCCC GGGTCGACCC ACGCGTCCGC GACGCCAACC CACACCAAAC	110	TICCTCAGCT TCTCTTCTCA AGACGGACGC CATTGGCAGC AGACAGACAG ACAGACAGAC	170	CCATAAAAGA GAGAGAGG GATCCATCGA ATGCGGCCAC CCTCC17TCA TCTTCGATTC	230	ATTACCATAC CATTCCGCTG ATCCATITIC CGCCTITICC GGGICTITICA TCCCAAAGGG	290	TATCCTITIC TATCCTATCT TCTCAAAGGG TCAGTCAGTT CCCTCCAATG CCTGCCGCCT	350	errecerser eserreceer everstags sserectrse escensears revaesteer	410	recaecete egaecetem eegeerreea retectete regeegaege ereteegee	470	GCCGGATTCT CYCCCAATGC GCCCCACTAC CTTCYGCITC CTCCGCCCYC CGCGGATCCA
40	ACGCGTCCGC	100	CATTIGGCAGC	160	NTGCGGCCAC	220	CGCCTTTTCC	280	TCAGTCAGTT	340	GGCTCCTTGC	400	тстсстстсс	. 460	crrcisciric
30	GGGTCGACCC	06	AGACGGACGC	150	GATCCATCGA	210	AICCATTING	270	TCTCAAAGGG	330	CICTGTACGT	390	CCGCCTTCCA	. 450	GCCCCACTAC
20	CGGNATICCC	80	TCTCTTCTCA	140	GAGAGAGAGG	200	CATTCCGCT'G	260	TATCCTATCT	320	cecrrccccr	380	свыссстст	440	CICCCAATGC
10	-A-CNTGGTC	70	Trccrcager	130	CCATAAAAGA	190	ATTACCATAC	250	TATCCTMYTC	310	crrcccrgcr	370	TCCACCCCTC	430	GCCGGATTCT

FIGURE 8

0 540	GTTTCCATAC CCTCGTCACC TCTTACCTCG CCTGCTTCGA GCCCTGCCAT GACTACTATA	009 0	CATCCGCATC CITIGITICGGA TCCAGACCCA TICGCACCAC CCGCAGGCAC CGGAGGCTCA	099 0	ATCGAGCTIC CCCTICCAGG GGAGGCAATG GCCGTGGCTC 16CAACCTGA ACAGGAAGTI	0 720	ACCACAMAGA AGANGCCAMG TATCAMACAG CGGCGAGTAG TYGTGACTGG AATGGGTGTG	780	GTGACTCCTC TAGGCCATGA ACCTGATGIT ITICTACAAT AATCTGCTTG ATGGAACGAG	340	TGGCATAAGC GAGATAGAGA CCTTTGAITIG TGCTCAAITT! CCIACGAGAA TTGCTGGAGA	006	GATCAAGICT ITCTCCACAG AIGGTTGGGT GGCCCCGAAG CTCICTAAGA GGATGGACAA	096 (GTTCATGCIN TACATGCTG TGCTGGCNN GNANGCATIN ACAGATGGTG GAATCACCGA	1020	AGATGIGATG AAAGAGCTAG AIAAAAGAAA ATGCGGAGTII CICAITTGGCT CAGCAAIGGG
530	GCCCTGCCA	, 590	CCCCAGGCA	029	TECAACCTE!	710	TIGIGACTG	770	AATCTGCTTC	830	CCTACGAGAA	068	CTCTCTAAGA	950	ACAGATGGTG	1010	CTCNTTGGCT
520	CCTGCTTCGA	580	TICGCACCAC	640	GCCGTGGCTC	700	CGGCGAGTAG	160	TTTCTACAAT	820	TGCTCAATTT	080	GCCCCGAAG	940	GAAAGCATTA	1000	ATGCGGAGTT
510	TCTTACCTCG	570	rccagaccca	630	GGAGGCAATG	069	TATCAMACAG	750	ACCTGATGIT	810	CCTTTGATTG	870	ATGGTTGGGT	930	CTGCTGGCAA	066	N'INNNAGNNA
200	CCTCGTCACC	260	CITIGITICGGA	620	CCCTTCCAGG	680	AGAAGCCAAG	740	TAGGCCATGA	800	GAGNTAGAGA	860	TTCTCCACAG	920	TACATGCTGA	980	NANGAGCTAG
490	GTTTCCAIAC	550	CATCCGCATC	610	ATCGAGCTTC	0.29	ACCACAAAGA	730	GTGACTCCTC	190	TGGCATAAGC	850	GATCAAGICT	910	GTTCATGC'FA	970	AGATGTGATG

FIGURE 8 2/5

NCCACATGAC	TGCGATGCCT	GAGTTFCACT	TTCTAGGTGG	TGCGACTATT TACGCAGANT TTCTAGGTGG GAGTTFCACT TGCGATGCCT ACCACATGAC	TGCGACTATT
1500	1490	1480	. 1470	1460	1450
NGANNAGAGG	GAGCATGCAA	AGAGGAGT'IG	TGCTACTACT	TATGGGGGAA GGAGCTGGAG TGCTACTACT AGAGGAGTTG GAGCATGCAA AGAAAAGAGG	TATGGGGGAA
1440	1430	1420	1410	1400	1390
ATGGATHTGT	AGTAATCGTG	ACCATGGGAC	AAGCITCAAG	GAGAAATTCC GACCCTACTA AAGCTTCAAG ACCATGGGAC AGTAATCGTG ATGGAMTGT	GAGAAATTCC
1380	1370	1360	1350	1340	1330
CTITIGICCCA	GCATGCCGAG	AGGITITIGITI	TYGGTATGGG	AGATGCGGTA ATCATACCTA TTGGTATGGG AGGTTTTGTT GCATGCCGAG CTTTGTCCCA	AGATGCGG'FA
1320	1310	1300	1290	1280	1270
GCGGGGGCTC	GIGATGCITTI	CGAAGCAGAT	TAATCAGAGG	ANTGANTGCT GCGAACCATA TAATCAGAGG CGAAGCAGAT GTGATGCTTT' GCGGGGGCTC	AATGAATGCT
1260	1250	1240	1230	1220	1210
ACTITITICIAL	GCAACGAGTA	racrectrer	ACTCGATATC	GGGATGGATG GGGCCCAACT ACTCGATATC TACTGCTTGT GCAACGAGTA ACTTTTGTAT	GGGATGGATG
1200	1190	1180	1170	1160	1150
CANTGGACTIT	GCIMIGCITIG	TINTEGGNTICA	CTACCACAAA	TCCCIPTTGI GTACCITTCG CIACCACAAA INTGGGAIICA GCIMIGCITIG CAAIGGACITI	TCCC'ITTTG'I
1140	1130	1120	1110	1100	1090
NGAAGNTGAA	ATTTCATATA	NGCCCTINAGG	NIGCCATIGA	TGGAATGAAG GTAFFCAATG AFGCCAFTGA AGCCCTAAGG AFFFCAFAFA AGAAGAFGAA	TGGAATGAAG
1080	1070	1060	1050	1040	1030

FIGURE 8

TITIGIGICCG	GCCCNTGAGT	CTCTAGACAT	GGACTCCAGC ATGITGGTAG CTCCITACGT CICIAGACAT GCCCAFGAGT 1TIGIGTCCC	ATGITGGTAG	GGACTCCAGC
2040	2030	2020	2010	2000	1990
GAAGTITITGA	CTACTCAACA TATCAAAGCT GAAGTTTTGA	CTACTCAACA	TTACATICTAG GACGTTTCGT GTGTCGAATT	GACGTTTCGT	TTACATICTAG
1980	1970	1960	. 1950	1940	1930
TCTTCGCCCC	TCGTCCATAC	TGGGCACAAC	GGTCGGTTTG ICTRAATTCAT TTGGGTTTTGG TGGGCACAAC TCGTCCATAC TCTTCGCCCC	TCTAATTCAT	GGTCGGTTTG
1920	1910	1900	1890	1880	1870
TGAACGTTAA	NAGGAGAGAC	GGGTCCTAAG	AGATOMAGGC GIGGATACAA AATIGCICGT GGGICCTAAG AAGGAGAGAC IGAACGTIAA	G'IGGATACAA	AGATGAAGGC
1860	1850	1840	1830	1820	1810
TGGNAAACCC	AA'FAT'FAATT	GNTCCATCCG	TICAGIAGIT CAGGCAATAA GGACIGGGTG GATCCAICCG AATAITAATT TGGAAAACCC	CAGGCAATAA	TTCAGIAGTT
1800	1790	1780	1770	1760	1750
TGGAAGCAGT	ccccrccrc	TCTCGGAGCA	TANTICAACC AAATCAATGA TIGGICACCII ICTCGGAGCA GCCGGTGGIG TGGAAGCAGT	ANATCANTGA	TANTICAACC
1740	1730	1720	1710	1700	1690
AGTTAAAAGT	CNAMICAGAG	Creitrices	AGATATCAAA GAGTACCAAG CTCTFATCCA CTGTTFCGGC CAAAACAGAG AGTFAAAAGT	GAGTACCAAG	AGATATCAAA
1680	1670	1.660	1650	1640	1630
כיוככפפכיוכם	GCCACATCCA	אאאיייראאא	AGGAGICTCI' AGGGAAGACG I'AAA'FI'ACAI' AAATGCCCA'I' GCCAGATCCA CTCCGGCTGG	AGGGAAGACG	AGGAGICTCI
1620	1610	1600	1590	1580	1570
TGGCTCAGTC	GAGAAGGCTT	TCTCTGCATA	CGAGCCTCAC CCTGATGGAG CTGGAGTGAT TCTCTGCATA GAGAAGGCTT TGGCTCAGTC	CCTGATGGAG	CGAGCCTCAC
1560	1550	1540	1530	1520	1510

FIGURE 8

	ı	ATCC	2370 GCTCTAGAGG	2350 2360 2370 AAAAAAAAA AAGGGGGGC GC'FC'FAGAGG ATCC	2350 NANAAAAAN
Trincicaaa	ITTGTGGTTT TAAAATTTGT AAAACTAGAA GACTGGTTTA GATTGGTTTG TTTTCTCAAA	GACTGGTTTIA	AAAACTAGAA	TAAAATTTGT	TTTGTGGTTT
2340	. 2330	2320	2310	2300	2290
TCATCACCGT	TOTTAACTCG GGCACGIAGT AACCAITIGG CCTTIGITIT GCTCTCTAIT TCATCACCGT	CCTTTGTTTT	AACCAITTIGC	GGCACGTAGT	TGTTAACTCG
2280	2270	2260	2250	2240	2230
AGAACAAAGC	CTCCTTGCAA TAGTIGIACT 'FTCGAGC'FFT I'CATCGAGTC AGTGAAGAAG AGAACAAAGC	TCATCGAGTC	rrcgagcmr	TAGTTGTACT	CTCCTTGCAA
2220	2210	2200	2190	2180	2170
TGAAATCTCC	כיואפאאדיפד יופפיואפאפכא איואיוירכאיויא יוכיוכאיואיוי יויויאיזייויכיוכ יופאאאיוכיוככ	TICTICATIATIF	איויזיאיזיאיזיא	TGGTINGNGCN	CTAGAATTGT
2160	2150	2140	2130	2120	2110
ATACTCCTTG	GAGCITTAGI CGGAACCATG ACGGAITGAG TACICATGGC GACACITGAI AIACTCCTTG	TACTCATGGC	ACGGATTGAG	CGGAACCATG	GAGC1TTAGF
2100	2090	2080	2070	2060	2050

FIGURE 8 5/5

Sequence Range: 1 to 1580

40 AMG GCG AAT GCA TCT GGG Met Ala Asa Ala Ser Gly>	90 100	GCA ACT CAG CAT TCG Ala Thr Glu His Ser>	140 150	GTC TCC AAA AGG GTG Val Ser Lys Arg Val>	190	G TCT TYG GGT GAT n Ser Leu Gly Asp>	240	GGA TGC AAA 'TTA ATT' GGA TCT Gly Cys Lys Leu Ile Gly Ser>	270 CAA GTC TCA AAT GAT GAT CTT GCT AAA Gln Val Ser Asn Asp Asp Leu Ala Lys>	0 340	CGA ACG GGG ATC CGC Arg Thr Gly Ile Arg>
40 A'NG GG Met A	O,	AGG G(Arg A)		TTT Phe		GAC AGG CAG Asp Arg Gln	230	TGC AA	280 AAT GAT Asn Asp	330	ACT GTC CGA Thr Val. Arg
10 20 30 40 CCTGAATCGG ATTCAAGAGA GAGTTTCGTT GCTGGG A'FG GCG AAT Met Ala Asn	80	C'IG AGA AGG Leu Arg Arg	130	TCG GAG Ser Glu	180	er GAC		NGA GGA Nrg Gly	GTC 'FCA Val Ser	320.	it ACT
30 TTCGTT	ω	CCT GCC (Pro Ala D		TCC		S GAT 1	220	3 AGT /		32	A TGG A
20 GA GAGT	70	GTT CC	120	GGA TCT Gly Ser	170	GTT CAG GAT TCT Val Gln Asp Ser	•	CT'r G'rG AGT AGA Leu Val Ser Arg	GCT CTT Ala Leu		GAC ACC AAT GAT GAA TGG ATT. Asp Thr Asn Asp Glu Trp Ile
2 CAAGAG	7	TCT TCA GTT Ser Ser Val		CGT		GCC Nla	0		260 A CCA (e Pro	310	C AAT'
10 3GG ATT		CTG GGT TC Leu Gly Se	110	TCA TCG TCT Ser Ser Ser	160	TGT AGT Cys Ser	. 210	TCG CCG Ser Pro	GCT AT Ala Il		GAC AC Asp Th
CTGAAT	09	TTT CTG Phe Leu	· . • • •	ATT TCA Ile Ser		TTT TGC Phe Cys	0	TCT CGC TCG CCG AGG Ser Arg Ser Pro Arg	250 GGT TCT GCT ATA CCA Gly Ser Ala Ile Pro	300	ATT GIC Ile Val
O		FG		4 н		£- 0.	200	F Q	Ō		ХH

FIGURE 9 1/5

390	GCA TCA Ala Ser>		AAT GAT' Asn Asp>		TTC GGC Phe Gly>	OCT TIG TO Leu>	580	TTN GTC Leu Val>	630	CTA GTG Leu Val>		CGG GGA Arg Gly>
	ACA AAT 1TA C Thr Asn Leu A	430	GAC GCA /	480	Crr	530 AAG AAT CCT Lys Asn Pro		GGT Gly		AAC AAT ATT C Asn Asn Ile L	019	ACC GAT C Thr Asp A
380	Asn	4	GAC		GAC	AAG Lys	-	TTG	620	AAT' Asn	·9	ACC Thr
	ACA Thr		GTA Val		GAG	ZO ZO Lys	570	GTG		ASO		TGG Trp
	C'M		CAG	470	CC'F Pro	520 TGC AAA A		TTT Phe		7 Trr Phe		GAC TGG Asp Trp
370	AAA GAT AGT Lys Asp Ser	420	GCA	•	TCT ACC CCT GAG GAC Ser Thr Pro Glu Asp	GGC		'rcc AGT GGA Cys Ser Gly	019	GGG GGT Gly Gly	099	TYR GTT (TYR Val)
'n	GN'F Asp		ATG Met		TCT	CTT. Leu	260	AGT Ser	61	$\begin{array}{c} GGG\\ G1Y \end{array}$	•	TYT TYT
	MM Lys		GAG Glu	460	TGT ACT Cys Thr	510 GCA Ala	<i>U</i> 1	'rcc Cys		GGT		CGG
	GG'I Gly	410	CTA	46	'rgr Cys	aaa Lys		GCA		aga Arg	650	TC1' Ser
360	CTC TCA GGT Leu Ser Gly	,	AAA GCT CTA GAG Lys Ala Leu Glu		ATG Met	500 CAG ATA TCG Gln Ile Ser	0	ACC GCT GCA Thr Ala Ala	009	A'TT AGA Ile Arg	9	GGT GCT GAT TCT CTT TCT CGG Gly Ala Asp Ser Leu Ser Arg
			MM Lys		TTC	500 ATA Ile	550	ACC Thr		CAC		rcı' Ser
	CGA AGG GTT Arg Arg Val	400	AGG Arg	450	GTT			ATT Ile		TGC	0	GAT
350	NGG. Arg	4	GCA		ATG Met	CCT		GAC	290	GCT	64	GCr
•			GCA	•	GAT	490 AGT GCT Ser Ala	540	TAC	LA	GCT GCT		GGT
	ASC		GAG	440	GTG Val	490 AGT G		TCT		TCA		ATT Ile

FIGURE 9 2/5

	'ICA Ser>	GAT Asp>	820	GTT Val>	870	AGG Arg>		CGC Arg>		AAG Lys>	GCA Ala>
	CAG	770 CAT AGC GAT His Ser Asp	83	GM Glu		CCA		TTC		CTT GGA	
720	G'I'G Val		٠	GAT Asp		CCA	910	GTA Val	096	CTr Leu	1(CAT His
	GTG Val	777G Leu		GAA	860	'ITT Phe	9	GAG		GCA Ala	CTF
	GCT GTA	760 TYTY GAT Phe Asp	810	ANA	ω	GAT ASP		GGT AAA GAG Gly Lys Glu		TCA GCA Ser Ala	ង ខ្ម
710	GCT	7 'I'I'I' Plie		ATC		AGA Arg		GGT Gly	950	TCA ATC GAA Ser Ile Glu	1000 17G C
	GGA G1y	GCT Ala		GCA Ala	850	A'rC Ile	006	AAC Asn	01	ATC Ile	TGG Trp
	GCT Nia	Trivi Phe	800	GCT	8	TCC		TGC ATC CAA ATG Cys Ile Gln Met		TCA	GAC Asp
700	GCT	750 CYC Leu	~	AAA		$\begin{array}{c} GGG \\ G1y \end{array}$		CAA	0	CAG Gln	990 ATC Ile
7	GAT	GGG G1y		CTA		AAT Asn	068	ATC Ile	940	CCT CAG Pro Gln	AAC Asn
	$\begin{array}{c} \text{GGA} \\ \text{G1} \end{array}$	GAT	190	CAT	840	CAT	۵	TGC Cys		GTG Val	TCC
	TTT Phe	740 GAG GAA Glu Glu	7.5	AGG Arg		GGA Gly		TCT Ser		TCT	980 AAT' GGA Asn Gly
069	CTC	GAG Glu		CM Gln		CTG	880	TCA TAC Ser Tyr	930	CGC	9 AAT' ASII
	ATT Ile	GCT		$\begin{array}{c} GGG\\ G1 \end{array}$	830	AAA GCC Lys Ala	88	TCA		TGC Cys	CTT
	TGT Cys	730 TGT GAT Cys Asp	780	GAT	ω	AMA		TCT		GCT	
680	ACA	73 TGT Cys		GGA Gly		GAT Asp		CGT	920	TTT Phe	970 GCC GGr Ala Gly

FIGURE 9 3/5

1060	TT CCT CAA	1110	Gr GCG GCA er Ala Ala>		AT GTG AAG sn Val Lys>	1200	TC ACA TGG eu Thr Trp>	0 1260	G CACITGCAGC'I	0 1320	TCCTCTCAAA CCGATGTFTC ACGAAATTT GCTTCCATGA CCANAAAAG AAGAAGTCAG	0 1380	TCTTTTATGG AGCAAGCAAC ACGACACGAT CTFCAFCACA TTGCCC1111T TCG111CCCCT
1050	ANT CAG AGG ATC ATT GAT GCA GTA GCA ACA CGT CTA GAG GTT Asn Gln Arg Ile Ile Asp Ala Val Ala Thr Arg Leu Glu Val	1100	GGG AAC ACT AGT GCG Gly Asn Thr Ser Ala	1150	GCA CTA GAC GAA GCT GTG AGG AGT GGA AAT GTG Ala Leu Asp Glu Ala Val Arg Ser Gly Asn Val	12	rrr GGC GCC GGA CTC Phe Gly Ala Gly Leu	1250	GGT TCT GCT ATT ATC AGG TGG GGA TAA GACTGAA GCCGAGCCAG Gly Ser Ala Ile Ile Arg Trp Gly ***>	1310	CANAMAAN	1370	TGCCC1111
Ĭ	Arg I		GGG 7		AGG A	1190	GGC G	1240	TGAA G	1300	אירפא כ	1360	CACA T
0	CA ACA la Thr	1090	CGA ATT ATC TCA AAC TTG GCA AAT TAC Arg Ile Ile Ser Asn Leu Ala Asn Tyr	1140	cr crc la val	-	GA Trr ly Phe		AA GAC		GCTPICC		CTFCAP
1040	GTN G Val N		GCA A		GAA G	80	GCA ACC GCA GGA Ala Thr Ala Gly	1230	GGA T	1290	TITIN	1350	ACGAT (
	T GCA p Ala	0 *	C TrG n Leu	1130	N GAC	1180	A ACC a Thr		G TGG g Trp		NCGYN		אכפאכז
1030	VIT GA	1080	CA AA		CA CT		TT GC le Al	0	TC AG	1280	Truc	1340	CAAC
	ATC A		ATC 1	02	TTG G	1170	CAC GTG ATT His Val Ile	1220	ATT A		CGATG		יפכעעפ
	AGG	1070	ATT' Ile	1120	TCC ATT CCC TTG Ser Ile Pro Leu	-			GCT	1270	MA MA	1330	rgg A
1020	CAG Gln	-	CGA		ATT		GGT Gly	1210	TCT	-	TCTC	Ä	ידידי
	AAT		GAA		TCC	1160	CCG	12	GGT		TCC		TCT

FIGURE 9 4/5

				1570 1580 AAAAAAAAA AAAAAAAAA	1570 AAAAAAAAA
AAAAAAAAAAA	ANNANANAAA	TTTGCTAAAA	ATGITTIATAT	GAGATGACAG CATAAACATC ATGITTIATAT ITTIGCTAAAA AAAAAAAAA AAAAAAAAAA	GAGNTGACAG
1560	1550	1540	1530	1520	1510
CGGGACATIFG	CAFFITIGICIF	GCITTITACTT	TAATTGTFICA	FAAGTTATTT GTTTCTTGTT TAATTGTTCA GCITTTACTT CATMTGTCT CGGGACAITG	'FAAGTTATT
1500	1490	1480	1470	1460	1450
TYGICCCCAA	ATAGTTTC1T	TACAATACCC	Trecrencha	TITICCATING TITGATGATI TIGCTGACAA TACAATACCC ATAGITITCIT TIGICCCCAA	TTCCATTAG
1440	1430	1420	1410	1400	1390

FIGURE 9 5/5

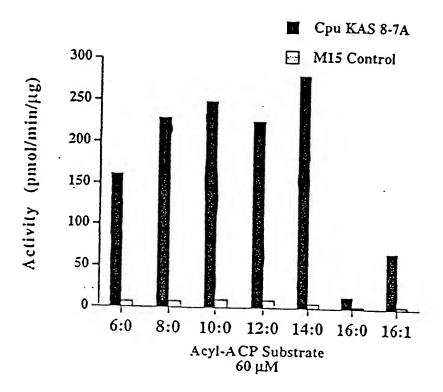


FIGURE 10

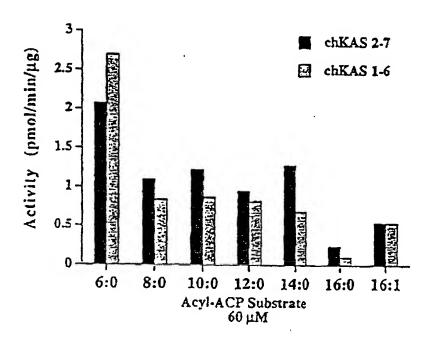


FIGURE 11

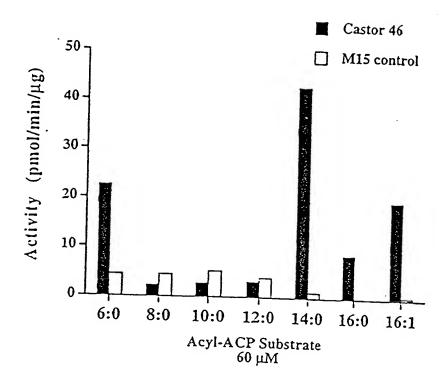
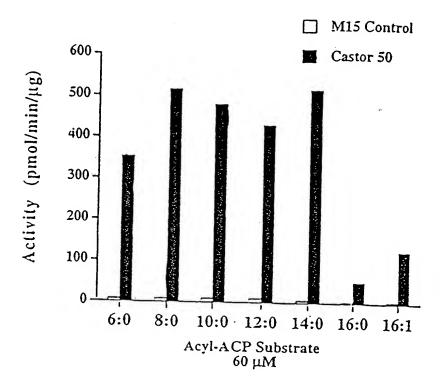


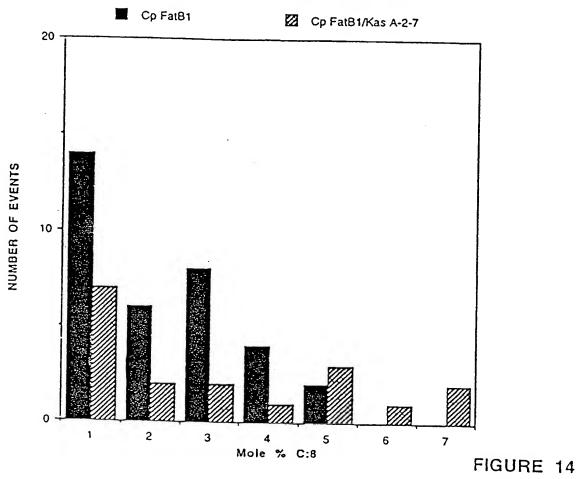
FIGURE 12

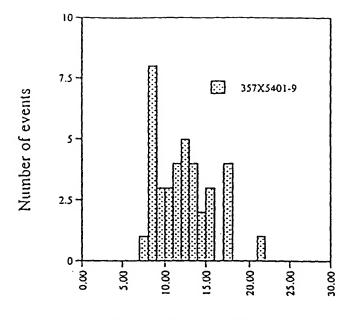


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FIGURE 13

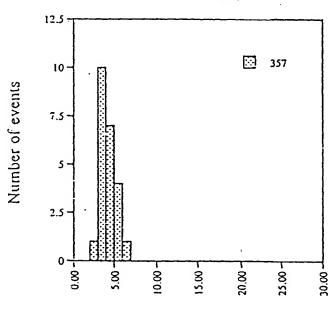
Cp FatB1 VS Cp FatB1/Kas A-2-7





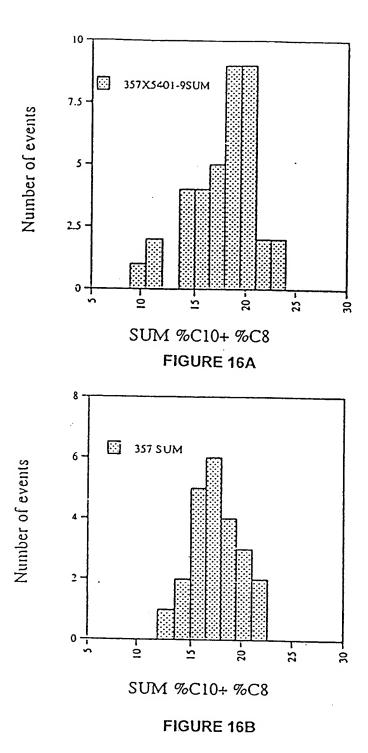
RATIO %C10 / %C8





RATIO %C10 / %C8

FIGURE 15B



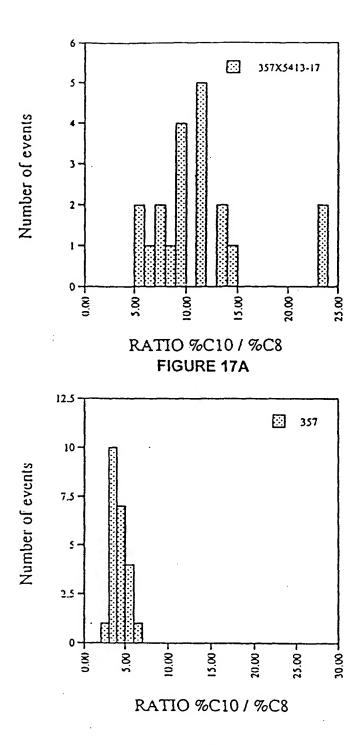


FIGURE 17B

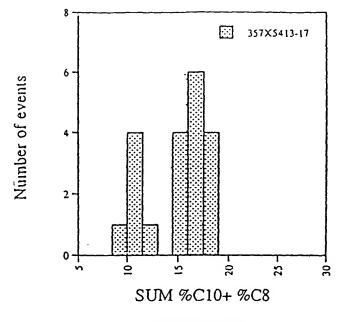


FIGURE 18A

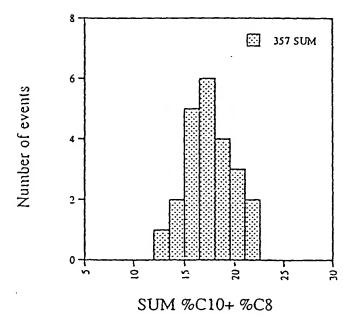
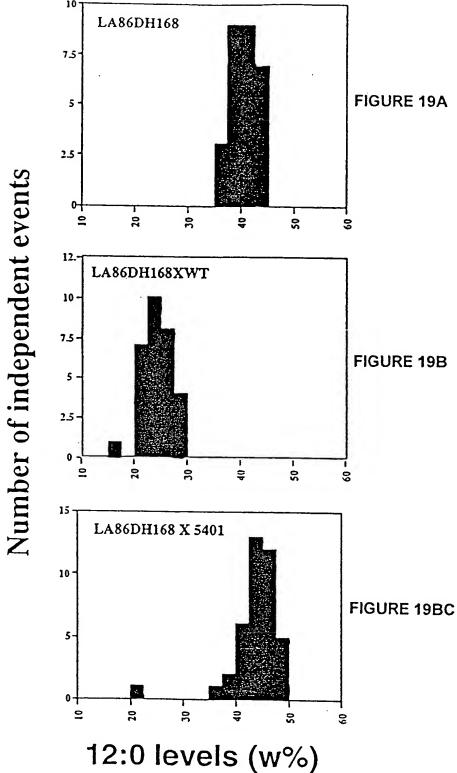


FIGURE 18B



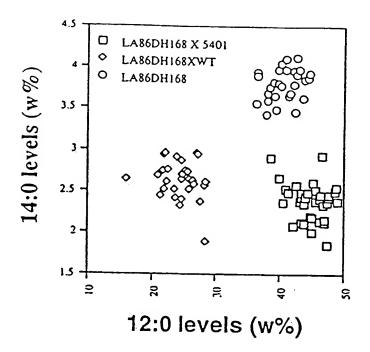


FIGURE 20

